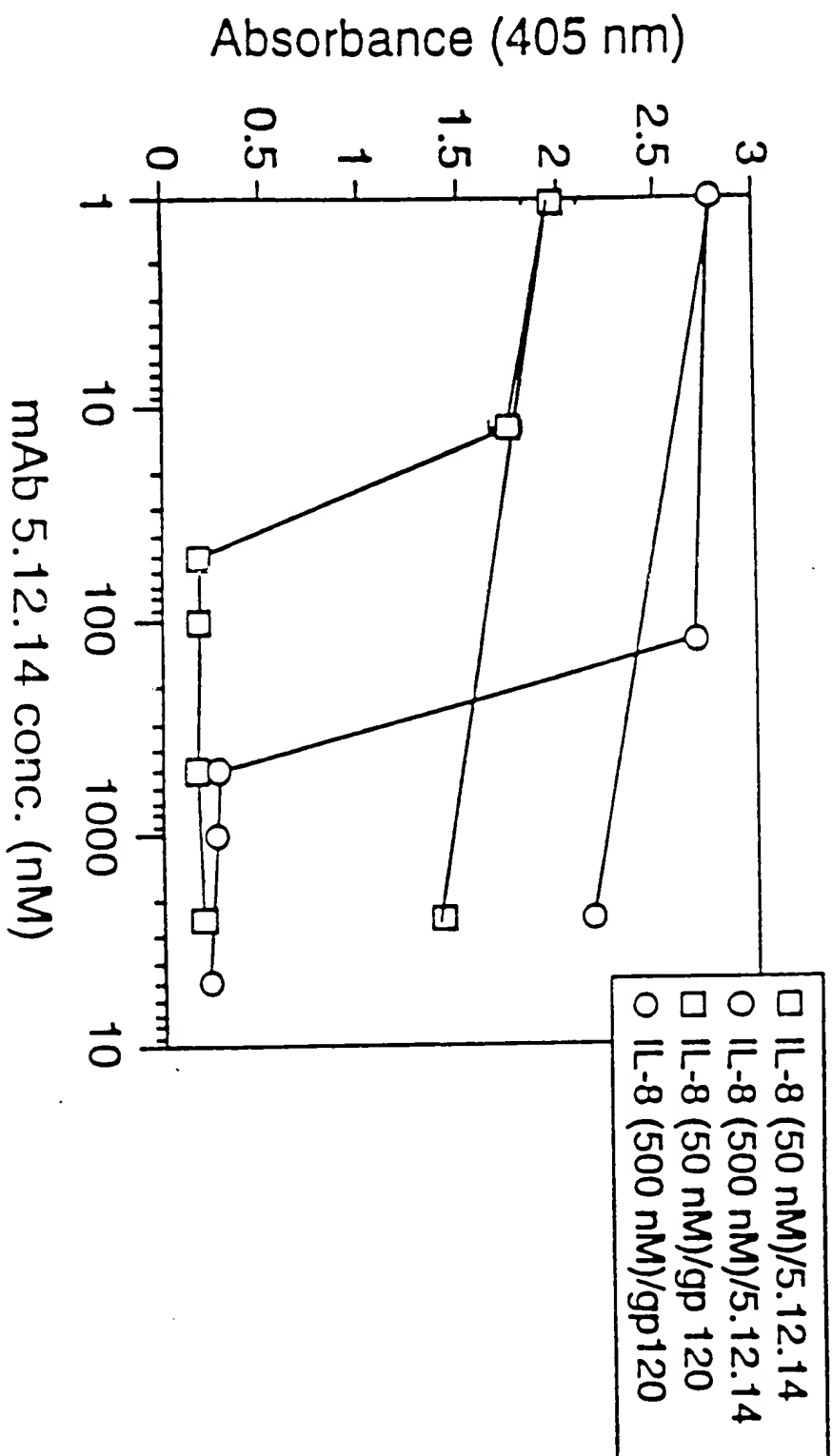
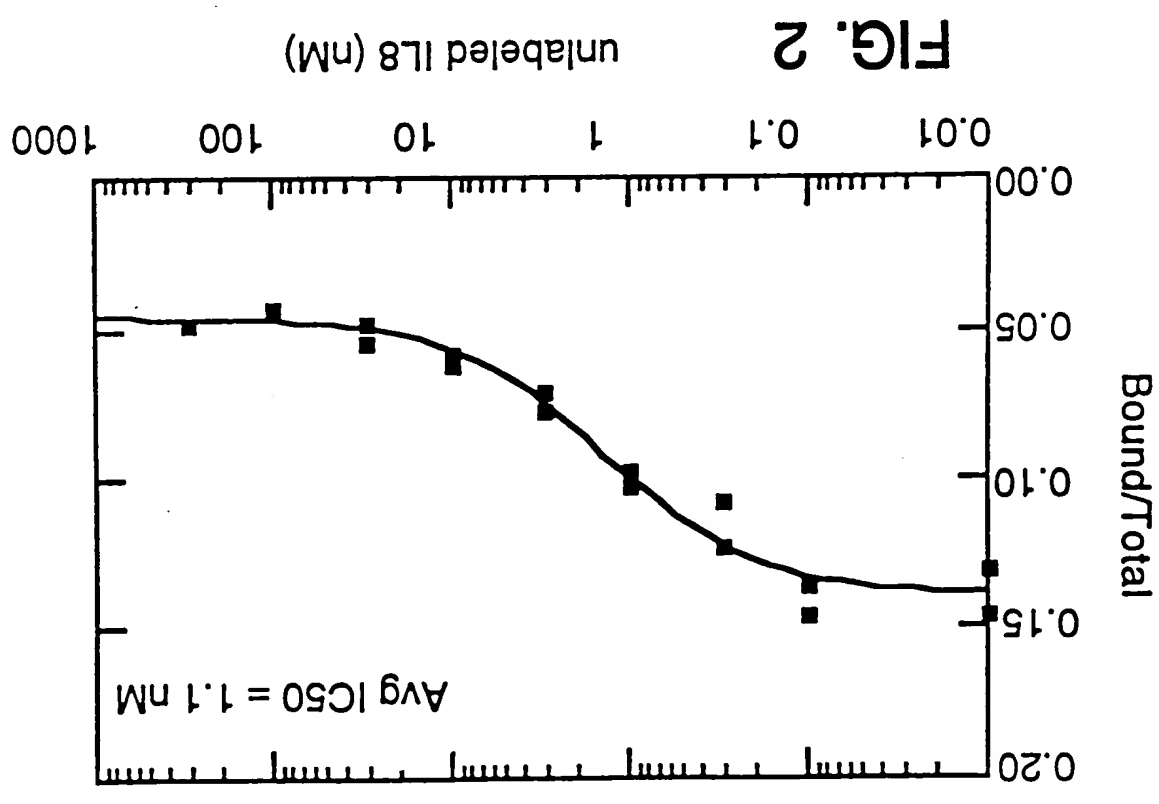
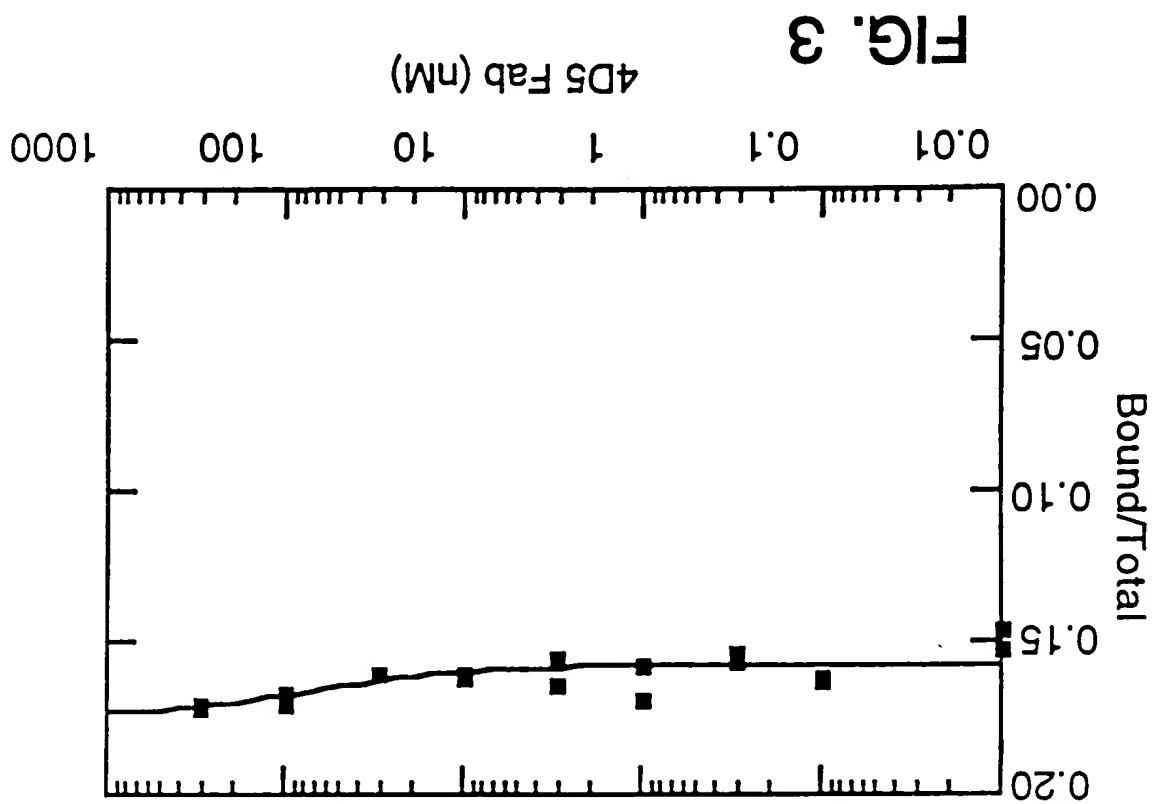
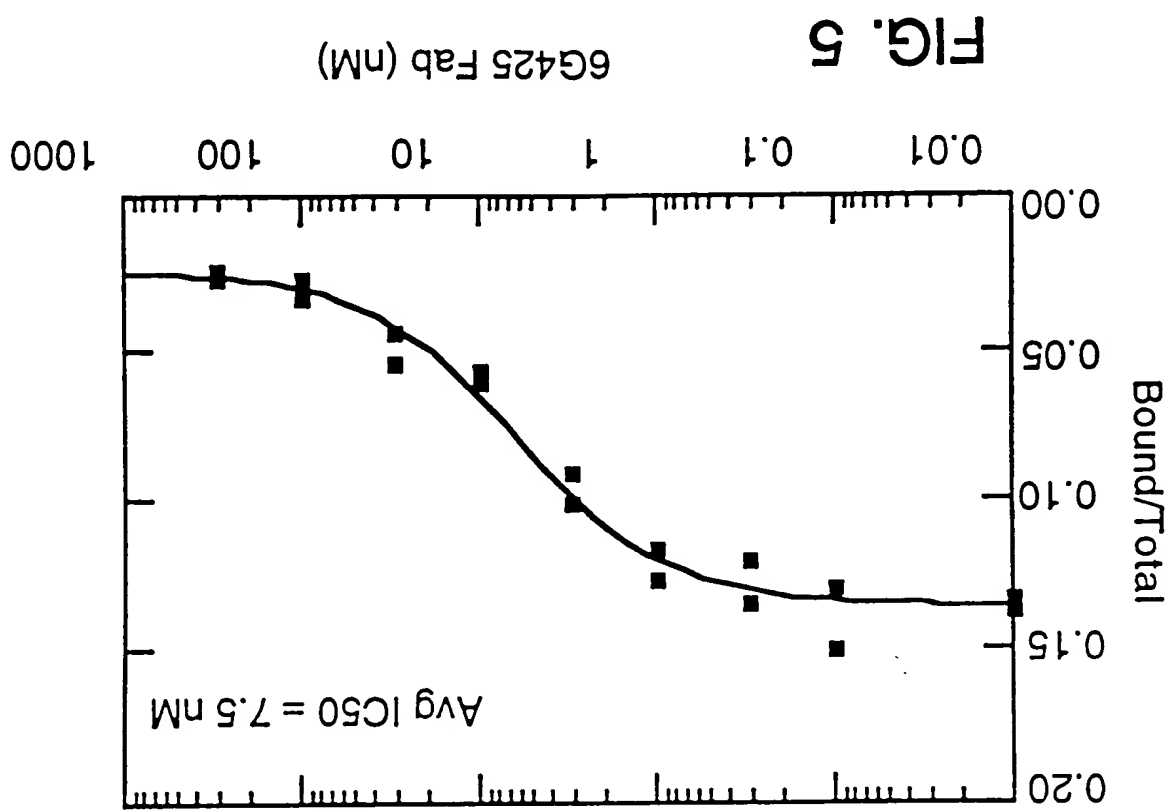
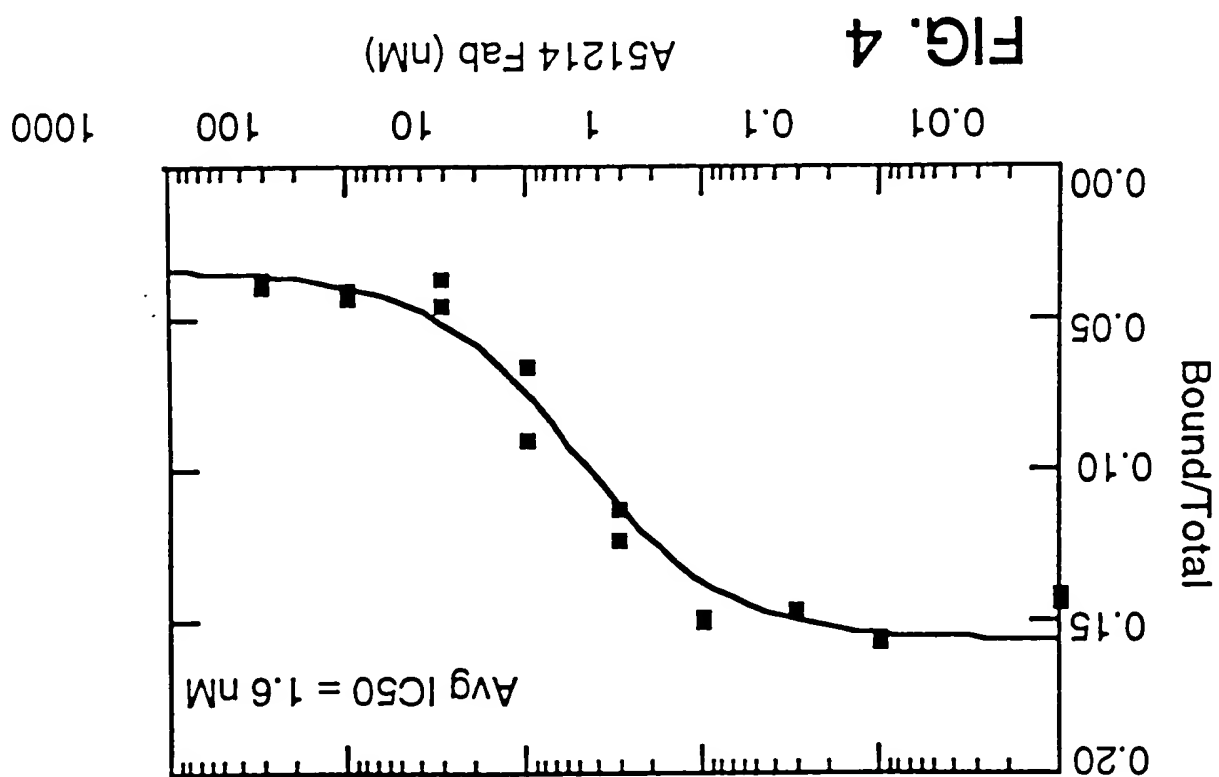


FIG. 1







**FIG. 6**

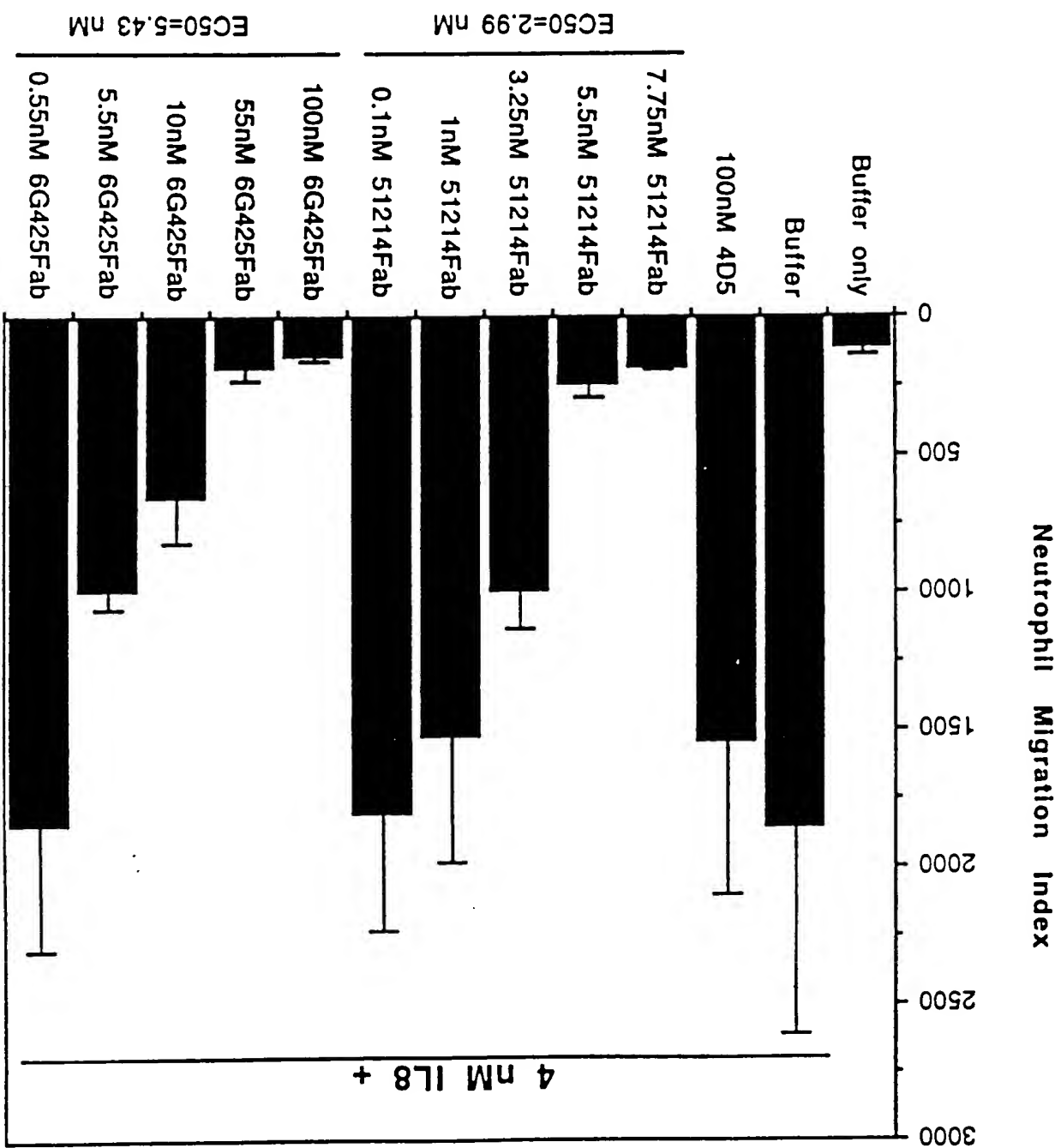


FIG. 7

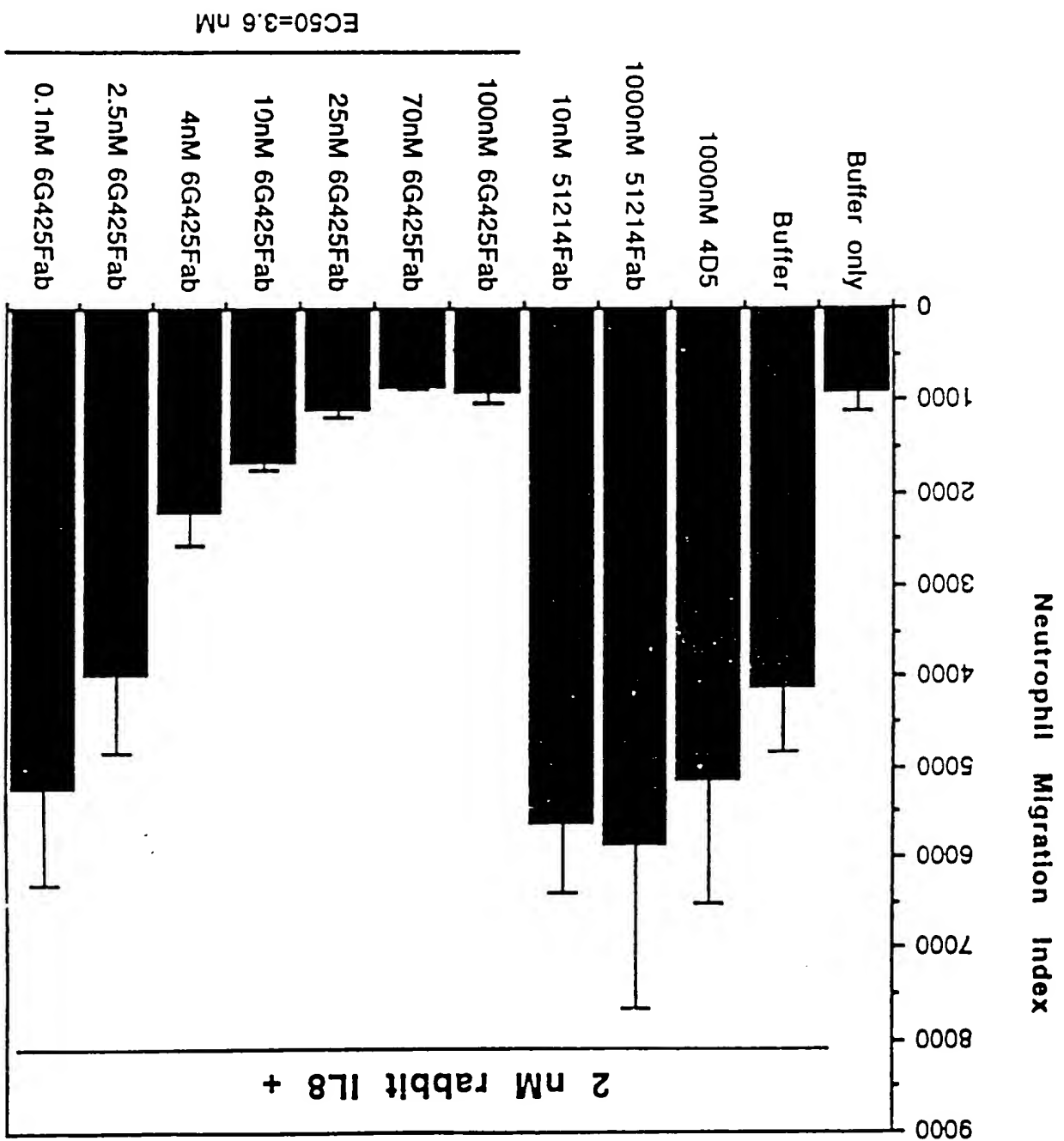


FIG. 8

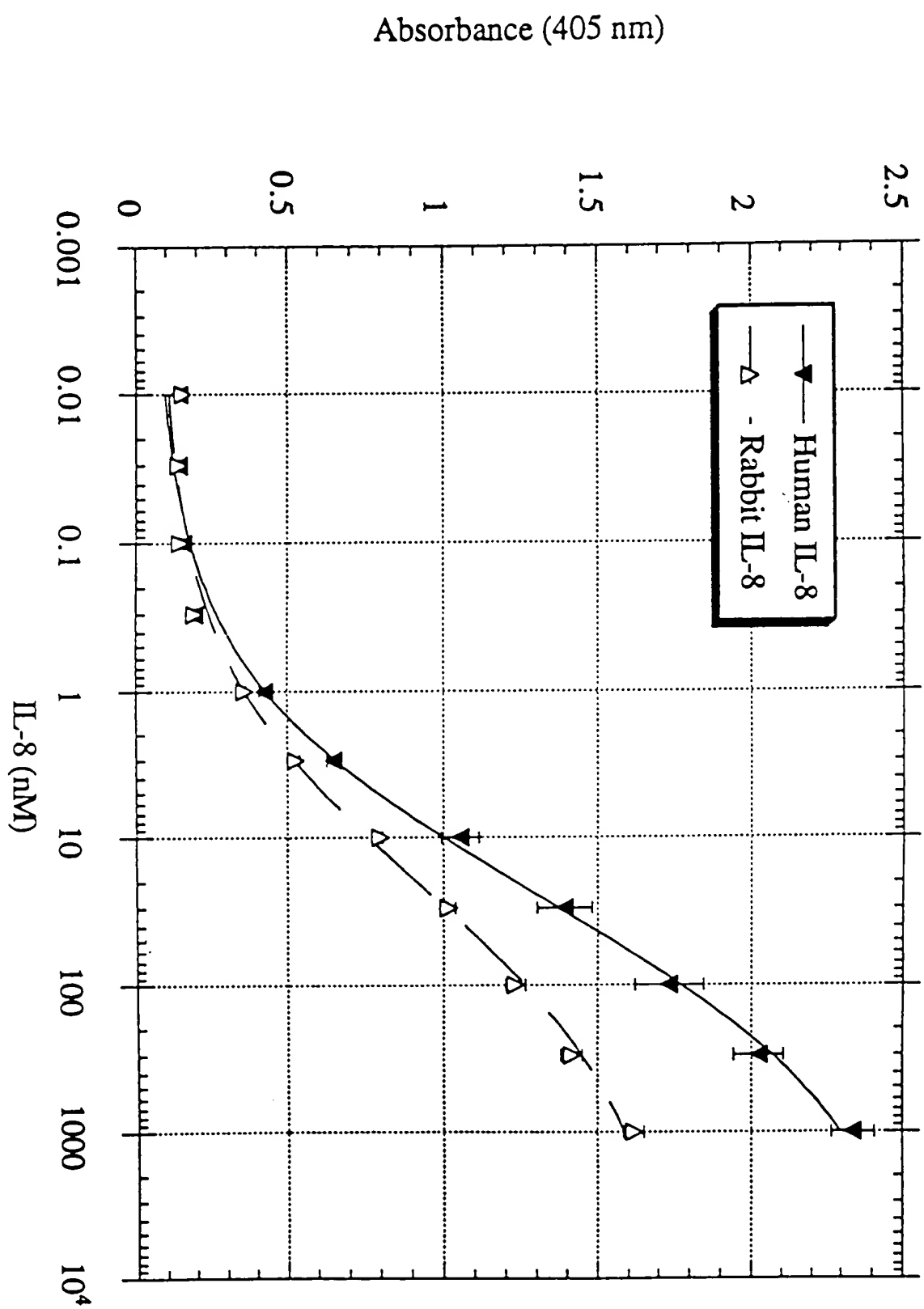
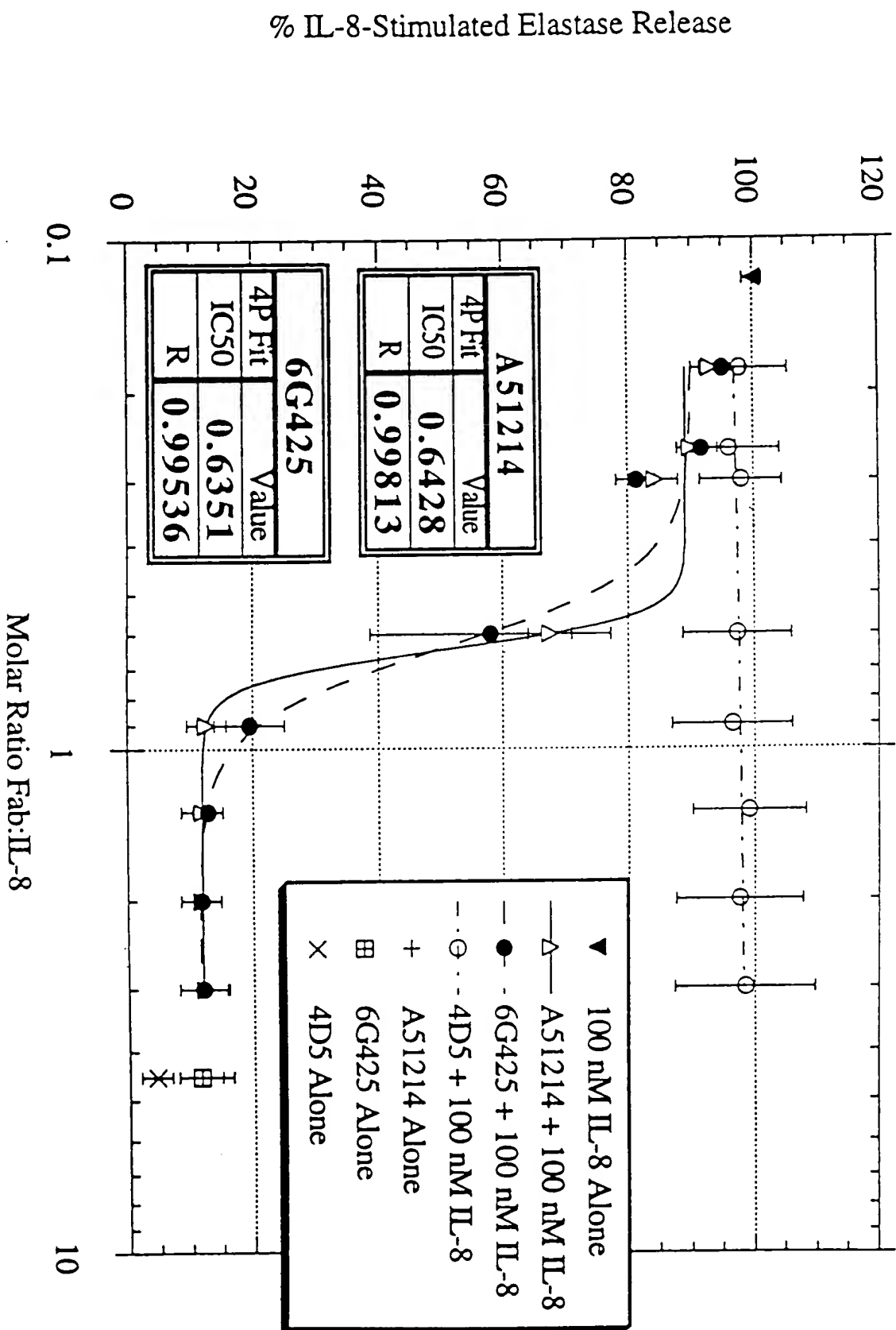
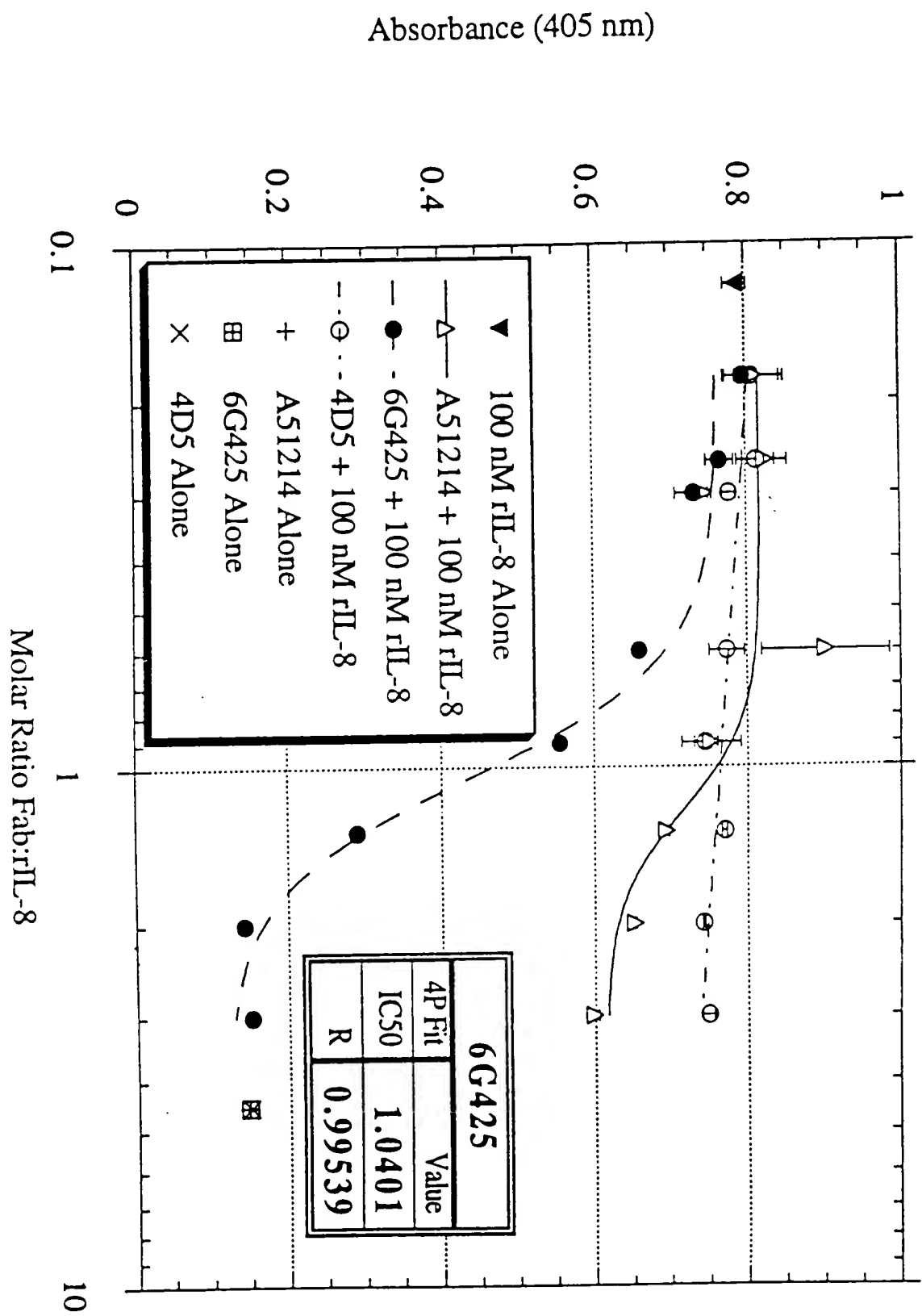


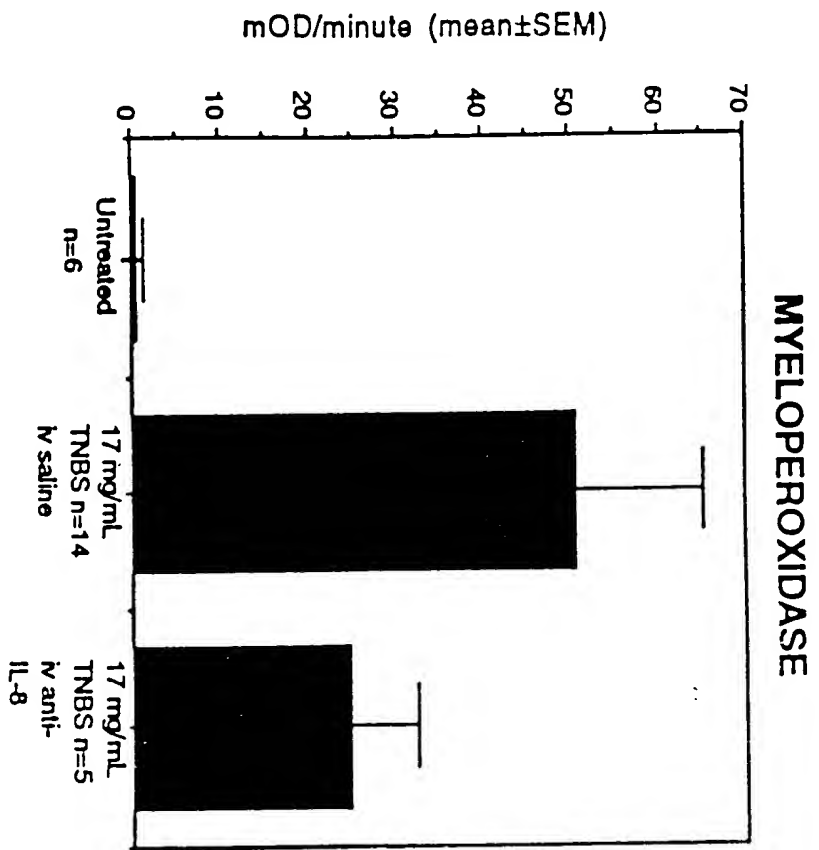
FIG. 9



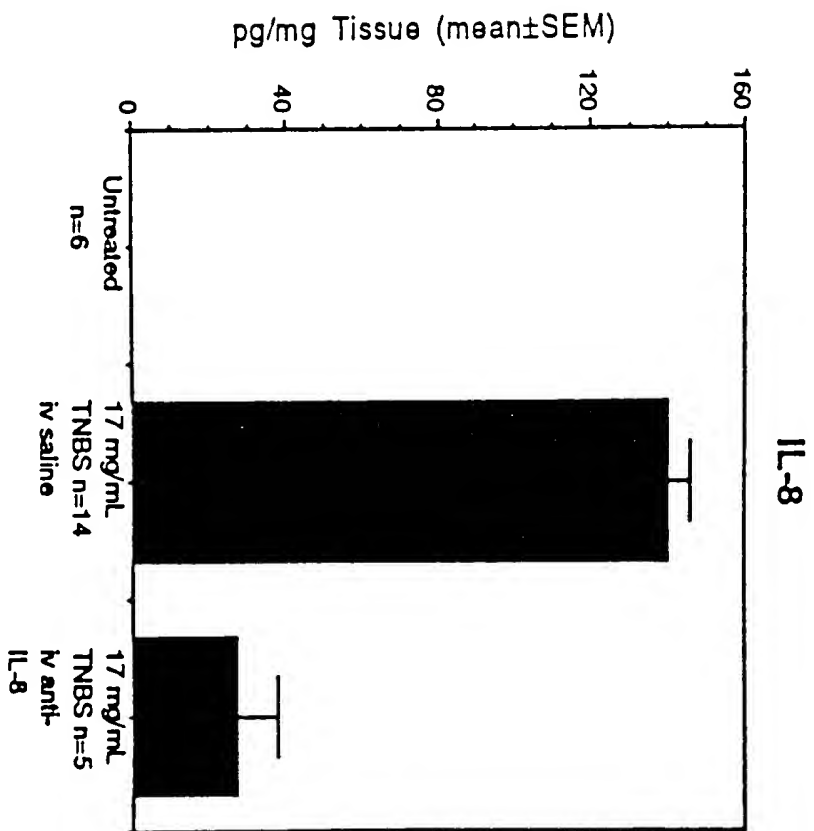
# FIG. 10



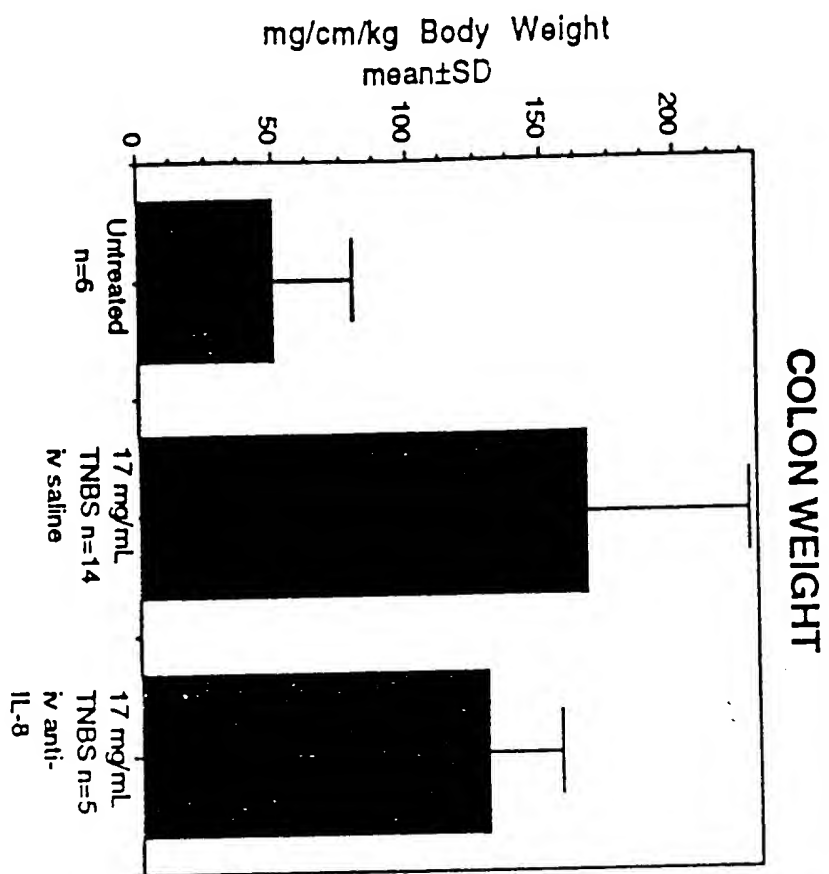




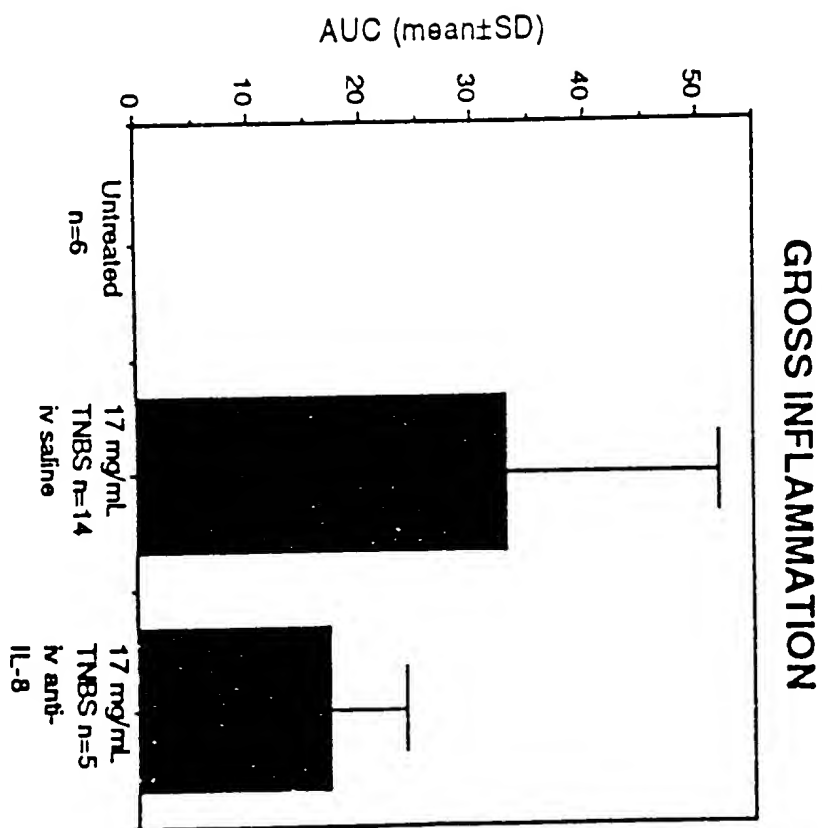
**FIG. 11A**



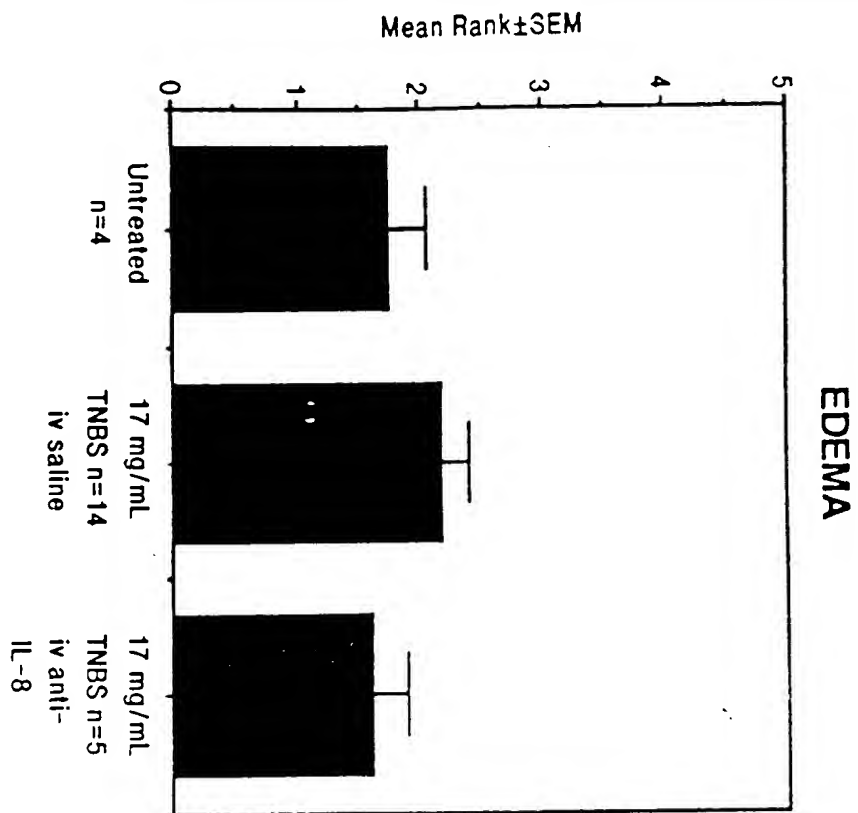
**FIG. 11B**



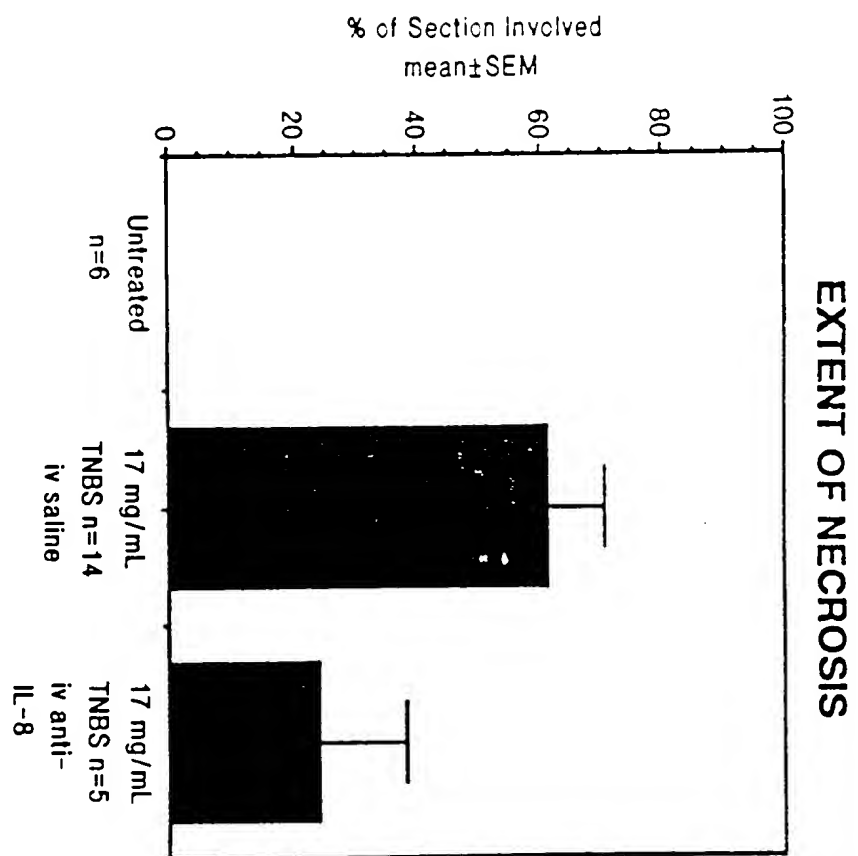
**FIG. 11C**



**FIG. 11D**



**FIG. 11E**



**FIG. 11F**

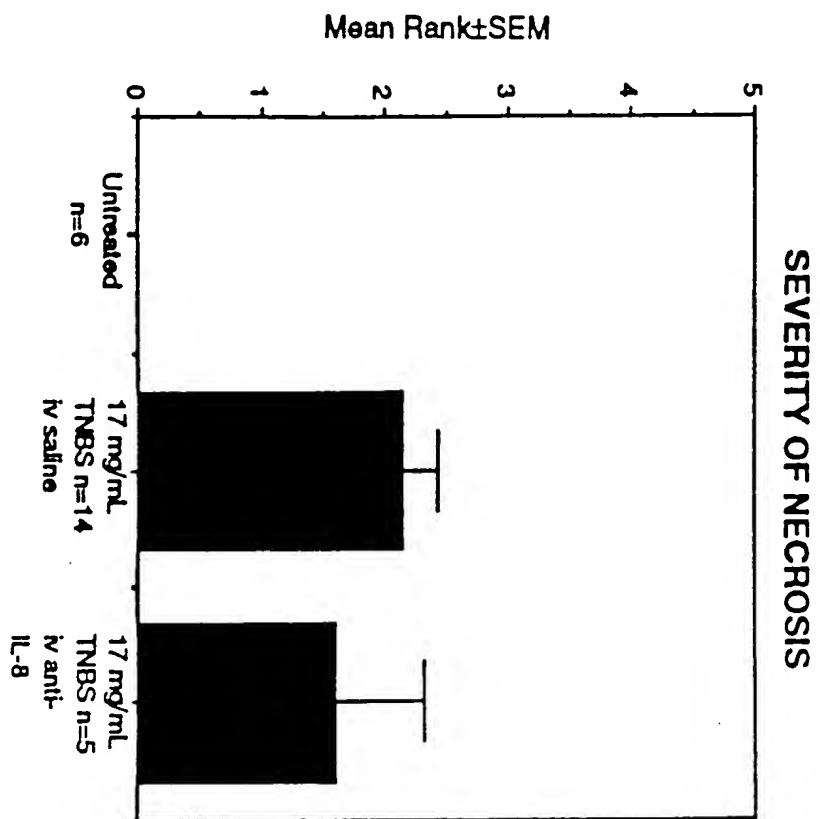


FIG. 11G

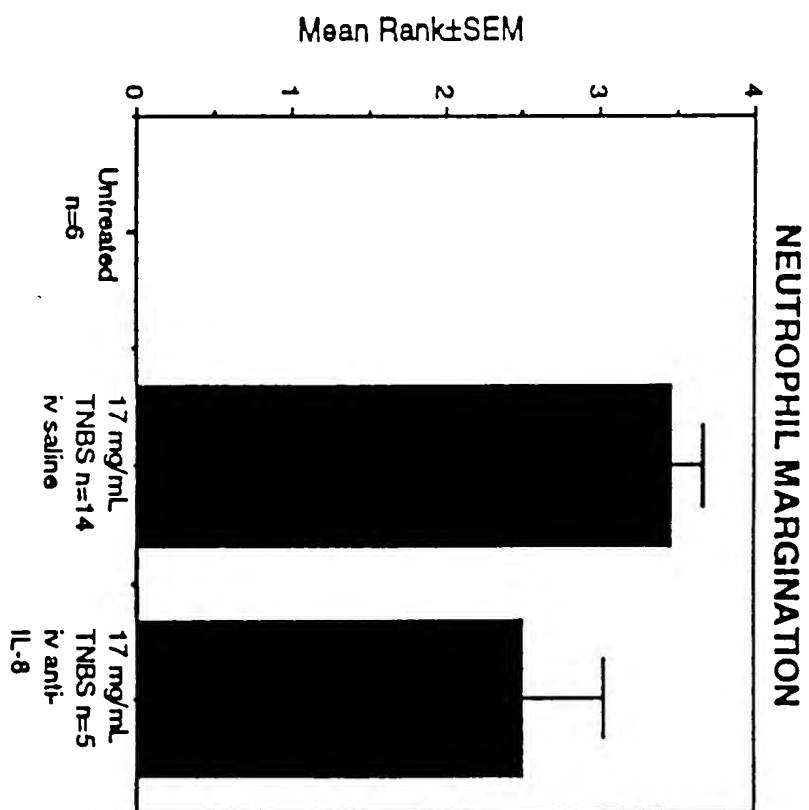


FIG. 11H

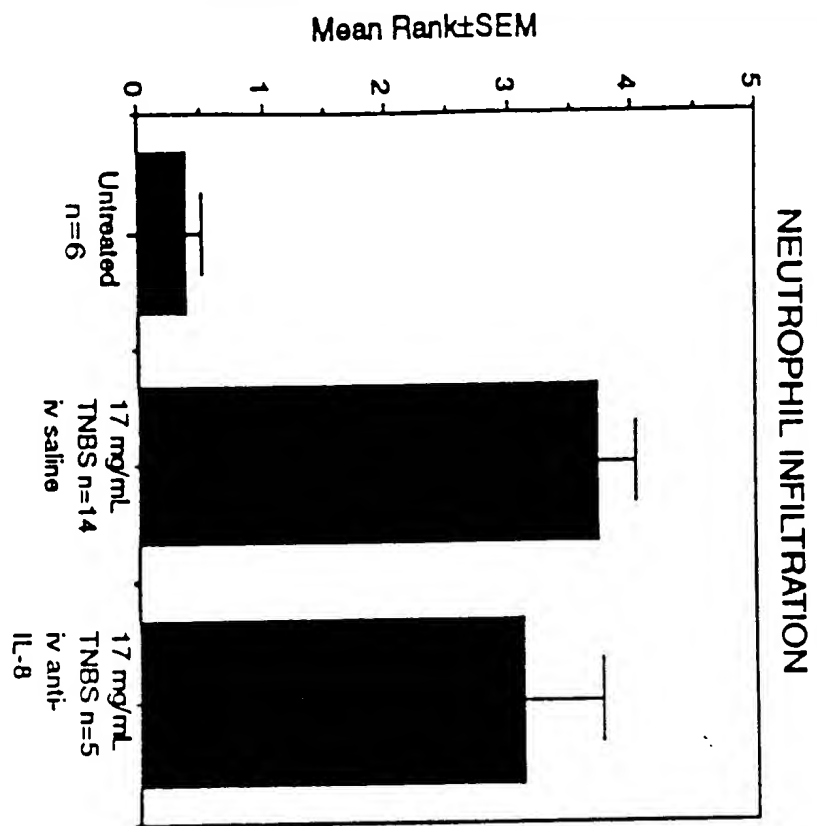


FIG. 11I

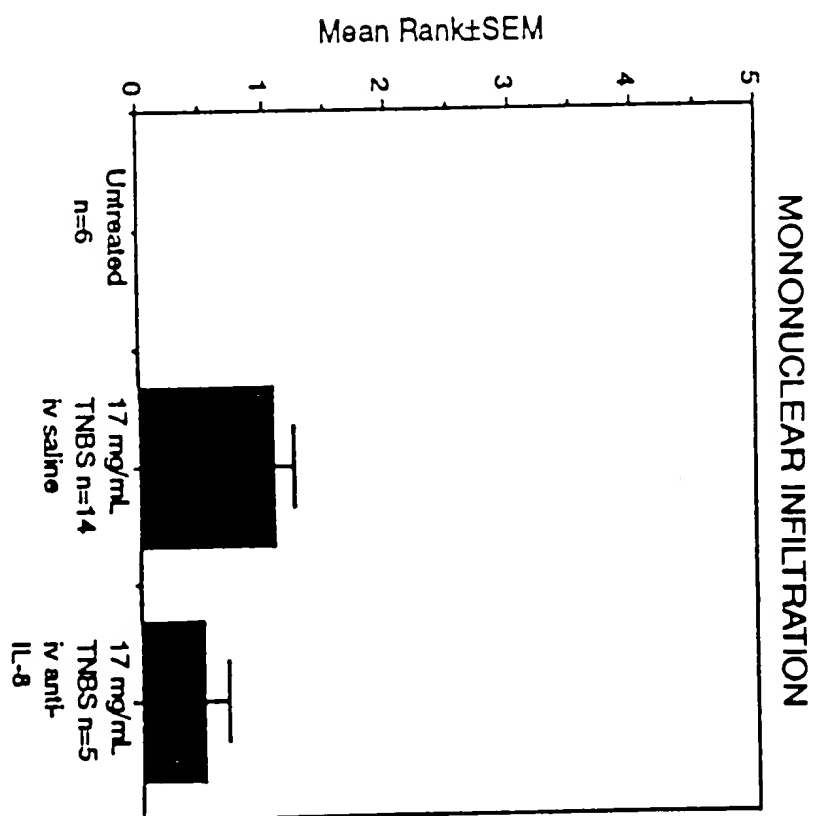
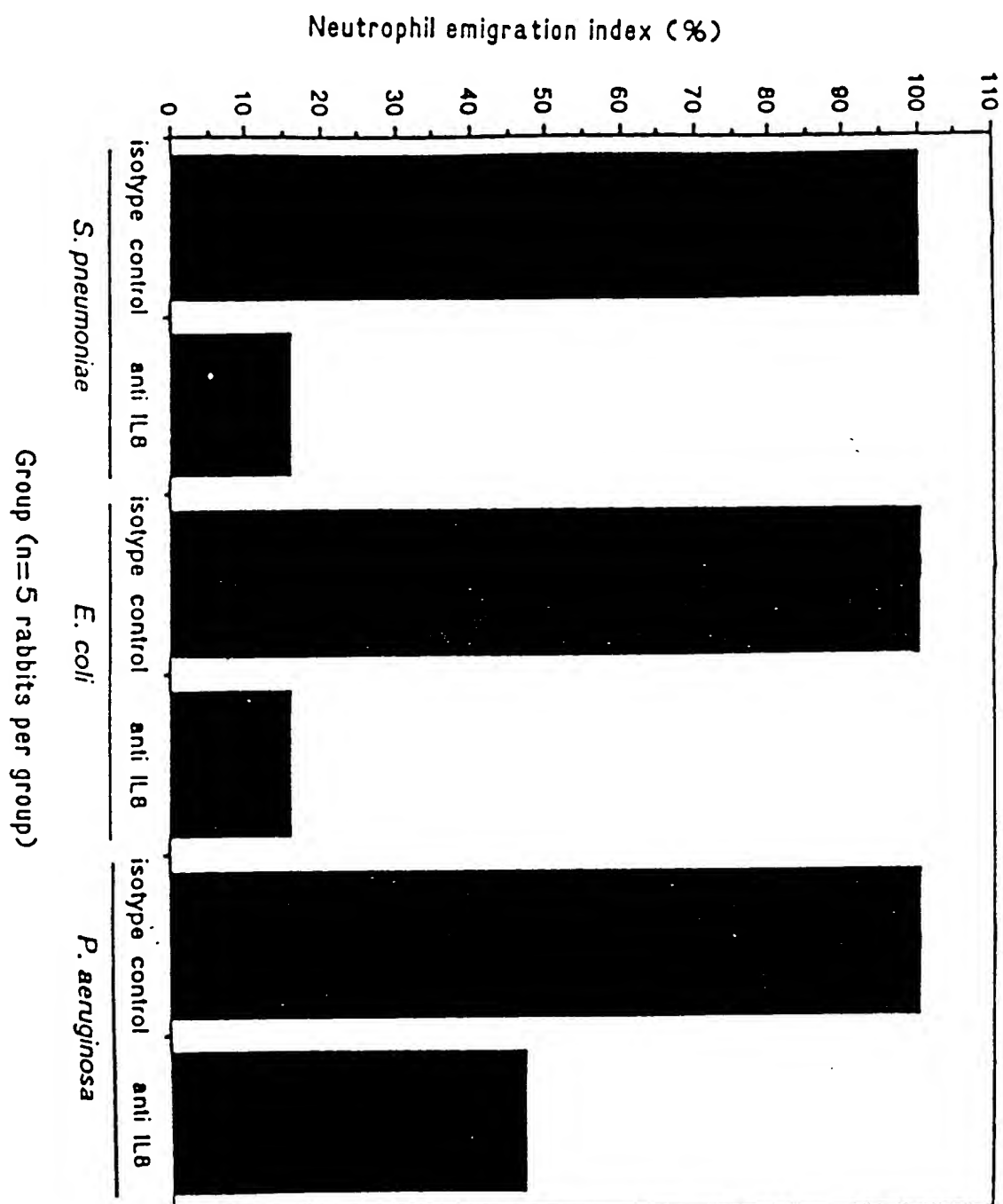


FIG. 11J

FIG. 12



Light chain Primers:

# FIG. 13

MKLC-1, 22mer

5' CAGTCCAACTGTTCAAGGACGCC 3'

(SEQ ID NO: 1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

(SEQ ID NO: 2)

MKLC-3, 23mer

5' GAAGTTGATGTTCTTGAGTGGC 3'

(SEQ ID NO: 3)

Heavy chain Primers:

IGG2A-1, 24mer

5' GCATCCTAGAGTCACCGAGAGCC 3'

(SEQ ID NO: 4)

IGG2A-2, 22mer

5' CACTGGCTCAGGGAATAACCC 3'

(SEQ ID NO: 5)

IGG2A-3, 22mer

5' GGAGAGCTGGGAGGCTGTGCAC 3'

(SEQ ID NO: 6)

FIG. 14

Light chain forward primer

SL001A-2 35 mer

5' ACAACCGGTACGCT GACATCGTCATGACCCAGTC 3'

A  
T

T T

Light chain reverse primer

SL001B 37 mer

5' GCTCTTCGAATG GTGGGAAGATGATACAGTTGGTGC 3'

(SEQ ID NO: 7)  
(SEQ ID NO: 8)  
(SEQ ID NO: 9)



Heavy chain forward primer

FIG. 15

SL002B 39 mer

5' CGATGGCCCCG ATAGACCGATGGGCTGTTGTTGGC 3' (SEQ ID NO:11)

(SEQ ID NO:12)  
(SEQ ID NO:13)  
(SEQ ID NO:14)

T  
G  
A

Heavy chain reverse primer

SL002B 39-MER

5' CGATGGCCCCG ATAGACCGATGGGCTGTTGTTGGC 3' (SEQ ID NO:11)

(SEQ ID NO:15)  
(SEQ ID NO:14)  
(SEQ ID NO:13)

T  
A  
G

1 GACATTGTCA TGACACAGTC TCAAAATTC ATGTCACAT CAGTAGGAGA CAGGTCAGC  
CTGTAACAGT ACTGTGTCAG AGTTTTTAAG TACAGGTGTA GTCATCCTCT GTCCAGTCG  
1 D I V M T Q S Q K F M S T S V G D R V S

61 GTCACCTGCA AGGCCAGTCA GAATGTGGT ACTAATGTAG CCTGTATCA ACAGAAACCA  
CAGTGACGT TCCGGTCAGT CTACACCCA TGATTACATC GGACCATAGT TGTCTTGGT  
21 V T C K A S O N V G T N V A W Y Q Q K P  
\* \* \* \* \*

#### CDR #1

121 GGGCAATCTC CTAAGCACT GATTTACTCG TCATCCTACC GGTACAGTGG AGTCCCTGAT  
CCCCTAGAG GATTTCTGA CTAATGAGC AGTAGGATGG CCATGTCACC TCAGGACTA  
41 G Q S P K A L I Y S S S Y R Y S G V P D  
\* \* \* \* \*

#### CDR #2

181 CGCTTCACAG GCAGTGATC TGGACAGAT TTCACTCTCA CCATCAGCCA TGTGCAGTCT  
GGAGAGTGC CGTCACCTAG ACCCTGTCTA AAGTGAGAGT GGTAGTCGGT ACACGTCAGA  
61 R F T G S G S G T D F T L T I S H V Q S

241 GAAGACTTGG CAGACTATT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCCT  
CTTCTGAACC GTCTGATAA GACAGTCGTT ATATTGTAGA TAGGAGAGTG CAAGCCAGGA  
81 E D L A D Y F C Q Q Y N I Y P L T F G P  
\* \* \* \* \*

#### CDR #3

301 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC CATCTTCCCA  
CCCTGGTTCG ACCTCAACTT TGCCCGACTA CGACGTGGTG GTTGACATAG GTAGAAGGCT  
101 G T K L E L K R A D A A P P T V S I F P

#### BstBI

361 CCATTTCGAA (see MD No: 16)  
GGTAAGCTT

121 P F E (see MD No: 17)

FIG. 16

1 TTCTATTGCT ACAACGCGT ACGCTGAGT GAGTCTGGG GAGCTTAACT  
1 AAGATAACGA TGTTGCGCA TCGCACTCCA CGTCGACCACT CACCAATCA

61 GCGGCGCTGA GGGTCCCTGA AACTCTCTG TGCAGCCTCT GATTCATAT TCAGTAGTTA  
13 P P G G S L K L S C A A S G F I F S S X

CDR #1

121 TGGCATGCT TGGTTGCGC AGACTCCAGG CAAGAGCCTG GAGTTGGTCG CAACCATTA  
33 G M S W V R Q T P G K S L E L V A T I N

181 TAATAATGGT GATAGCACT ATTATCCAGA CAGTGTGAAG GCGCGATTCA CCATCTCCCG  
53 N N G D S T Y Y P D S V K G R F T I S R

CDR #2

241 AGACAATGCC AAGAACCCT TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC  
73 D N A K N T L Y L Q M S S L K S E D T A

301 CATGTTTAC TGTGCAAGG CCTCATTAAG TTCGGCTACT TGGTTGGTT ACTGGGCGCA  
93 M F Y C A R A L I S S A T W F G Y W G Q

CDR #3

361 AGGACTCTG GTCACTGCT CTGCAGCCAA AACAAACGCC CCATCTGCT  
113 G T L V T V S A A K T T A P S V Y

ApaI

411 ATCCGGG (Seq ID No: 18)  
130 TAGGCC P (Seq ID No: 19)

FIG. 17

# FIG. 18

VL.front	31-MER	5' <u>ACAAAGCGTACCGCTGATATCGTCATGACAG</u>	3' (SEQ ID NO: 26)
VL.rear	31-MER	5' <u>GCAGCATCAGCTCTTCGAAGCTCCAGCTTGG</u>	3' (SEQ ID NO: 21)
VH.front	SPE	21-MER	5' <u>CCACTAGTACGCAAGTTACG</u>
VH.rear	33-MER	5' <u>GATGGGCCCTTGCTGGAGGCTGCAGAGACAGTG</u>	3' (SEQ ID NO: 23)

1	ATGAAGAAGA	ATATCGCAT	TCTCTTGA	TCTATGTTG	TTTTTCTAT	TCCTACAAC
-23	M K K N	I A F	L L A	S M F V	F S I	A T N
61	GCCTACGCTG	ATATCGCAT	GACACAGTCT	CAAAATTCA	TCTCCACATC	AGTAGGAGAC
-3	A Y A D	I V M	T Q S	Q K F M	S T S	V G D
121	AGGGTCAGCG	TCACCTGCAA	GGCCAGTCAG	AATGTGGTA	CTAATGTAGC	CTGGTATCAA
121	TCCTAGTCCG	AGTGGACGTT	CCGGTCAGTC	TTACACCCAT	GATTACATCG	GACCATAGTT
18	R V S V	T C K	A S O	N V G T	N V A	W Y Q
CDR #1						
181	CAGAAACCAG	GGCAATCTCC	TAAAGCACTG	ATTACTCGT	CATCCCTACC	GTAACAGTGA
38	Q K P G	Q S P	K A L	I Y S S	S Y R	Y S G
CDR #2						
241	GTCCTGATC	GCTTCACAGG	CAGTGGATCT	GGGACAGATT	TCACTCTCAC	CATCAGCCAT
58	V P D R	F T G	S G S	G T D F	T L T	I S H
301	GTGAGTCTG	AAGACTTGCC	AGACTATTTC	TGTACAGCAAT	ATAACATCTA	TCCTCTCAGC
78	V Q S E	D L A	D Y F	C Q Q	X N I Y	P L T
CDR #3						
361	TTCGGTCTCG	GGACCAAGCT	GGAGCTTCGA	AGAAGCTGTG	CTGCACCATC	TGTCTTCATC
98	F G P G	T K L	E L R	R A V A	A P S	V F I
421	TTCGCCCAT	CTGATGAGCA	GTTGAAATCT	GGAATCTGTT	CTGTTGTGTC	CCTGCTGAAT
118	F P P S	D E Q	L K S	G T A S	V V C	T L N
481	AACCTCTATC	CCAGAGAGGC	CAAGATACAG	TGGAAGGTGG	ATAACGCCCT	CCAATCGGGT
138	N F Y P	R E A	K V Q	M K V D	N A L	Q S G
541	AACTCCAGG	AGAGTGTAC	AGAGCAGGAC	AGCAAGGACA	GCACCTACAG	CCTCAGCAGC
158	N S Q E	S V T	E Q D	S K D S	T Y S	L S S
601	ACCCTGACGC	TCAGCAAGC	AGACTACGAG	AAACACAAAG	TCTACGCCCTG	CGAAGTCAAC
178	T L T L	S K A	D Y E	K H K V	Y A C	E V J
661	CATCAGGGCC	TCAGCTCGCC	CGTCACAAAG	AGCTTCAACA	GGGAGAGTGG	
198	H Q G L	S S P	V T K	S F N R	G E C	
711	TTAA					
216						

# FIG. 20A

1 ATGAAAAGA ATATCGATT TCTTCTTGA TCTATGTTG TTTTTCAT TCCTACAAAC  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 CGGTACGCTG AGTGCAGCT GGTGAGTCT GGGGAGGCT TAGTCCGCT TGAGGGTCC  
 -3 A Y A E V Q L V E S G G G L V P P G G S  
 121 CTGAACCTCT CCTGTGCAGC CTCTGATTG ATATTGAGTA GTTATGGCAT GTCTTGGGTT  
 18 L K L S C A A S G F I F S S X G M S W V  
 CDR #1  
 181 CGCCAGACTC CAGGCAAGAG CCTGAGATTG GTCCGAACA TTAATAATAA TGGTGATAGC  
 GCGGTCTGAG GTCCGTCTC GGACCTCAAC CAGCGTTGCT AATTATTAT ACCACTATCG  
 38 R Q T P G K S L E L V A T I N N N G D S  
 241 ACCTATTATC CAGACAGTGT GAAGGGCCGA TTCACCATCT CCGGAGACAA TGCCAGAAC  
 TGGATATAG GTCTGTACA CTTCGCGCT AAGTGGTAGA GGGCTCTGTT ACGGTTCTTG  
 58 T Y Y P D S V K G R F T I S R D N A K N  
 CDR #2  
 301 ACCGTGTACC TGCAATGAG CAGTCTGAG TCTGAGGACA CAGGCATGTT TTACTGTGA  
 TGGACATGG ACGTTACTC GTCAAGACTC AGACTCCGTGT GTCCGTTACAA AATGACAGT  
 78 T L Y L Q M S S L K S E D T A M F Y C A  
 361 AGAGCCCTCA TTAGTTCGGC TACTTGTTT GTTACTGGG GCCAAGGAG TCTGGTCACT  
 TCTCGGAGT AATCAAGCCG ATGAACCAA CCAATGACCC GGGTTCCTG AGACCAAGTA  
 98 R A L I S S A T W F G Y W G Q G T L V T  
 CDR #3  
 421 GTCTCTGAG CCTCCACAA GGGCCCATCG GTCTTCCCC TGCCACCTC CTCCAAGAG  
 CAGAGAGTC GGAGGTGTT CCCGGTAGC CAGAAAGGGG ACCGTGGAG GAGGTTCTCG  
 118 V S A A S T K G P S V F P L A P S S K S  
 481 ACCTCTGGG GCACAGCGG CCTGGGCTG CTGGTCAAG ACTACTTCC CGAACCGGTG  
 TGAGAGCCCG CGTGTCCCG GGACCCGACG GACCAAGTCC TGATGAAGG GCTTGGCCAC  
 138 T S G G T A A L G C L V K D Y F P E P V  
 541 ACGGTGCTT GGAATCAGG CCGCTGACC AGCGGCTG ACACCTTCC GGTGTCTTA  
 TGCCACAGCA CCTTGAGTCC GCGGAGTGG TCGCCGACG TGTGAAAGG CCGACAGAT  
 158 T V S W N S G A T T S G V H T F P A V L  
 601 CAGTCTCAG GACTCTACTC CCTCAGCAGC GTGTGACCG TGCCCTCCAG CAGCTTGGG  
 GTCAGGAGTC CTGAGATGAG GGAGTCTCG CACCACTGGC ACGGAGGTC GTGAAACCCG  
 178 Q S S G L Y S L S S V V T V P S S L G

# FIG. 20B

661 ACCGACCT ACATCTGCAA CGTGAATCAC AAGCCCAAGCA ACACCAAGGT GGACAAGAAA  
TGGTCTGGA TGTAAGCGTT GCACTTAGTG TTCGGGTCGT TGTGGTTCCA CCTGTTCTTT  
198 T Q T Y I C N V N H K P S N T K V D K K  
721 GTTGAGCCCA AATCTTGTGA CAAACTCAC ACATGA (SEQ ID NO: 26)  
CAACTCGGGT TTAGAACACT GTTTGAGTG TGTAAT (SEQ ID NO: 27)  
218 V E P K S C D K T H T O

# FIG. 21

## Light Chain Primers:

MKLC-1, 22mer

5' CAGTCCAACTGTTGAGGAGCC 3'

(SEQ ID NO: 1)

MKLC-2, 22mer

5' GTGCTGCTCATGCTGTAGGTGC 3'

(SEQ ID NO: 2)

MKLC-3, 23mer

5' GAAAGTTGATGTTCTGTGAGTGGC 3'

(SEQ ID NO: 3)

## Heavy Chain Primers:

IGG2AC-1, 24mer

5' GCATCCCTAGAGTCAGCCGAGGAGCC 3'

(SEQ ID NO: 4)

IGG2AC-2, 22mer

5' CACTGGCTCAGGGAATAAACC 3'

(SEQ ID NO: 5)

IGG2AC-3, 22mer

5' GGAGAGCTGGGAAGGTGTCAC 3'

(SEQ ID NO: 6)



# FIG. 22

5' AGA TGT CAA TTG CTC ACT GGA TGG TGG GAA GAT GG 3' (SEQ ID NO: 31)  
 6G4.light.Mun 35-MER

Light chain reverse primer

5' CCAATGCATACGCT GAC ATC GTG ATG ACC CAG ACC CC 3' (SEQ ID NO: 28)  
 T T T A A  
 (SEQ ID NO: 29) (SEQ ID NO: 30)

6G4.light.Nsi 36-MER

Light chain forward primer

# FIG. 23

Heavy chain forward primer  
 6G4.heavy.Mlu 32-MER  
 5' CAACCGGTACGCT GAG ATC CAG CTG CAG CAG 3' (SEQ ID NO: 32)  
 (SEQ ID NO: 33)

Heavy chain reverse primer  
 SL002B 39-MER  
 5' CGATGGGCCCCG ATAGACCGATGGGCTGTTTGGC 3' (SEQ ID NO: 11)  
 (SEQ ID NO: 15)  
 (SEQ ID NO: 14)  
 (SEQ ID NO: 13)

T  
 A  
 G

# FIG. 24

70 G ATATCGTGAT GACACAGACA CCATCTCCG TGCCGTGACG TCTTGAGAT  
C TATAGCACTA CTGTGCTGT GGTGAGAGG AGGACAGTC AGAACCTCTA  
I D I V M T Q T P L S L P V S L G D

121 CAGGCTCCA TCTCTGAC ATCTAGTAC AGCCTGTAC ACGTATG AACAACCTAT  
GTCCGGAGGT AGAGACGTC TAGATCAGTC TCGAACATG TGCCATAACC TTTGTGATA  
18 Q A S I S C R S S O S L V H G I G N T Y

CDR #1

181 TTACATTGGT ACCTGAGAA GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTCC  
AATGTAACA TGACGCTCTT CGGTCCGGTC AGAGGTTTC AGGACTAGAT GTTCAAGG  
38 L H W Y L Q K P G Q S P K L L I Y K V S

CDR #2

241 AACGATTTT CTGGGCTCC AGACAAGTTC AGTGCAGTG GATCAGGAC AGATTTTACA  
TTGGCTAATA GACCCAGGG TCTGTCCAG TCACCGTAC CTAGTCCCTG TCTAAGTGT  
58 N R F S G V P D R F S G S G S G T D F T

301 CTAGGATCA GCAGAGTGA GCCTGAGAT CTGGACTTT ATTTCTGCTC TCAAGTACA  
GAGTCCCTAGT CGTCTCACT CCGACTCCTA GACCTGAAA TAAAGACGAG AGTTTCATGT  
78 L R I S R V E A E D L G L Y F C S Q S L

CDR #3

361 CATGTTCCCG TCACGTTCCG TGCTGGACC AAGCTGGAGC TGAAGAAGGC TGATGCTGA  
GTACAAAGCG AGTGCAAGCC ACGACCTGG TTCGACCTCG ACTTTGCCCG ACTACGACGT  
98 H V P L T F G A G T K L E L K R A D A A

MunI

421 CCAACTGTAT CCATCTTCCC ACCATCCAGT GAGCAATTGA  
(SEQ ID NO: 34)  
GGTTGACATA GGTAGAAGG TGGTAGGTCA CTCGTTAACT  
118 P T V S I F P P S S E Q L K  
(SEQ ID NO: 35)

# FIG. 25

70 G AGATTCAGCT GCAGCAGTCT GCACCTGAGC TGATGAAGCC TGGGCTTCA  
 C TCTAAGTCGA CGTCGTCAGA CCTGCACTCG ACTACTTCGG ACCCGAAGT  
 1 E I Q L Q S G P E L M K P G A S

121 GTGAAGATAT CCTGCAAGCC TTCTGGTTAT TCATTCAAGTA GCCACTAAT GCACCTGGGTG  
 CACTTCTATA GGACGTTCCG AAGACCAATA AGTAAGTCAT CGGTGATGTA CGTGACCCAC  
 18 V K I S C K A S G Y S F S H Y M H W V

CDR #1

181 AAGCAGAGCC ATGGAAGAAG CCTTGAGTGG ATTGGCTACA TTGATCCCTC CAATGGTGAA  
 TTCGTCTCGG TACCTTTCTC GGAACCTCAC TAACCGATGT AACTAGGAAG GTTACCACTT  
 38 K Q S H G K S L E W I G Y I D P S N G E

CDR #2

241 ACTACTTACA ACCAGAAATT CAAGGGCAGG GCCACATTGA CTGTAGACAC ATCTTCAGC  
 TGATGAATGT TGGTCTTTAA GTTCCCGTTC CGGTGTAAT GACATCTGTG TAGAAGGTG  
 58 T T Y N Q K F K G K A T L T V D T S S S

301 ACAGCCACAG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGA  
 TGTCCGTTGC ACGTAGAGTC GTCCGACTGT AGACTACTGA GACGTCAGAT AAAGACACGT  
 78 T A N V H L S S L T S D D S A V Y F C A

361 AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG TCTGGGGCCG AAGGACACAG  
 TCTCCCTGA TATCTATGTT GCCCGTGACC AAAAAGCTAC AGACCCCGCG TCCCTGGTGC  
 98 R G D Y R Y N G D W F F D V W G A G T T

CDR #3

421 GTACCCGCTCT CCTCCGCCAA AACCGACAGC CCCATCGGTC TATCCGGGCC  
 CAGTGGCAGA GGAGCGCGGAT TTGGCTGTGG GGTAGCCAG ATAGGCCCGG  
 118 V T V S S A K T D S P I G L S G P

471 CATC (SEQ ID NO: 36)  
 GTAG  
 135 I (SEQ ID NO: 37)

BstEII  
 ApaI

## FIG. 26

5' CTTGGTGAGCGCGGAGAGACG 3' (see ID no: 38)

SYN.Apa 22 MER

5' GTACCCGTCT CCTCCGCTC CACCAAGGC C 3' (see ID no: 40)

SYN.BstEII 31 MER

5' GAACGGGCTGTGCTGCACCACTGTATTCATCTCC 3' (see ID no: 39)

DS/VF 38MER

Mutagenesis Primer for 6G425VL

5' CTTGGTGAGCGCGGAGAGACG 3' (see ID no: 38)

# FIG. 27A

1 ATGAAGAAGA ATATCCGATT TCTTCTGCA TCTATGTTCCG TTTTTCAT TGCTACAAT  
 TACTTCTCT TATAGCGTAA AGAAGAAGCT AGATACAAGC AAAAAGATA ACGATGTTA  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCC TGCTGTCAG TCTTGAGAT  
 CGTATCGGAC TATAGCACTA CTGTGTCTGT GGTGAAGGG ACGACAGTC AGAACCTTA  
 -3 A Y A D I V M T Q T P L S L P V S L G D  
 121 CAGGCTCCA TCTCTTGCA ATCTAGTCA AGCTTGATC AGGTATGG AAACACCTAT  
 GTCCGAGGT AGAAGACGTC TAGATCACTC TCAGAACATG TGCCATTAAC TTGTGATA  
 18 Q A S I S C R S S O S L V H G I G N T Y  
 CDR #1  
 181 TTACATTGGT ACCTGCAGAA GCCAGGCCAG TCTCCAAGC TCCTGATCTA CAAAGTTCC  
 AATGTAAACA TGACGCTTT CGGTCCGGTC AGAGGTTCC AGGACTAGAT GTTCAAGG  
 38 L H W Y L Q K P G Q S P K L L I Y K V S  
 CDR #2  
 241 AACGATTT CTGCGTCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTCACA  
 TTGCTAATAA GACCCAGGG TCTGTCCAAG TCACCGTAC CTAGTCCCTG TCTAAGTGT  
 58 N R F S G V P D R F S G S G S G T D F T  
 301 CTCAGATCA GCAGAGTGA GGTGAGAT CTGGACTTT ATTCTGCTC TCAAGTACA  
 GAGTCCTAGT CGTCTCACT CGGACTCTA GACCTGAAA TAAAGAGAG AGTTTCATGT  
 78 L R I S R V E A E D L G L Y F C S Q S L  
 CDR #3  
 361 CATGTTCCG TCACGTTCCG TGCTGGACC AAGCTGAGC TGAACGGGC TGTTGCTGA  
 GTACAAGGG AGTCCAAGC ACGACCTGG TTGCACTCG ACTTGCCCG ACAAGCAGCT  
 98 H V P L T F G A G T K L E L K R A V A A  
 421 CCACTGTAT TCATCTTCC ACCATCCAGT GAGCAATTGA AATCTGGAAC TGCTCTGT  
 GGTGACATA AGTGAAGGG TGTTAGTCA CTGTTAATC TTAGACCTG ACGAGACAA  
 118 P T V F I F P P S S E Q L K S G T A S V  
 481 GTGCTCTG TGAATACTT CTATCCAGA GAGGCCAAG TACAAGTGA GGTGATTAAC  
 CACACGGAG ACTTATTGA GATAGGTTCT CTCGGTTCT ATGTACCTT CCACTATG  
 138 V C L T N N F Y P R E A K V Q W K V D N  
 541 GCCCTCAAT CGGTAACTC CCAAGAGAGT GTCAAGAGC AGGACAGCA GACAGCACC  
 CGGAGGTTA GCCCATGAG GGTCTCTCA CAGTGTCTG TCCTGTCTG CCTGTCTG  
 158 A L Q S G N S Q E S V T E Q D S K D S T  
 601 TACAGCTCA GACGACCT GACGTGAGC AAAGCAGCT ACGAAGAA CAAAGCTTAC  
 ATGTCCGAGT CGTCCGAGG CTGCGACTCG TTCCGCTGA TGCTCTTGT GTTTCAGATG  
 178 Y S L S S T L T L S K A D Y E K H K V Y

661 GCCTGCCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
 CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCTCCT  
 198 A C E V T H Q G L S S P V T K S F N R G

721 GAGTGTTAA (SEQ ID NO: 41)  
 CTCACAATT  
 218 E C O (SEQ ID NO: 42)

FIG. 27B

# FIG. 28A

1 ATGAAAAGA ATATCGATT TCTTCTGCA TCTATGTTG TTTTCTAT TGCTAACAAC  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCGTACGCTG AGATTCACT GCAGCAGCT GCACCTGAGC TGATGAAGC TGCGGCTTCA  
 -3 A Y A E I Q L Q Q S G P E L M K P G A S  
 121 GTGAAGATAT CCTGCAAGC TTCTGGTAT TCATTCACTA GCACTACAT GCACCTGGTG  
 CACTCTATA GCAGCTTCCG AAGACCAATA AGTAAGTAT CGGTATGTA CGTGACCCAC  
 18 V K I S C K A S G Y S F S S H Y M H W V  
 CDR #1  
 181 AAGCAGAGC ATGAAAGAG CCTGAGTG ATTGGCTACA TTGATCCTT CAATGGTGA  
 TTGCTCTCG TACCTTTCTC GGAATCACC TAACCGATG AACTAGGAAG GTTACCACTT  
 38 K Q S H G K S L E W I G Y I D P S N G E  
 CDR #2  
 241 ACTACTTACA ACCAGAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC  
 TGATGAATGT TGGTCTTAA GTTCCCGTTC CGGTGTAAT GACATCTGTG TAGAAGGTG  
 58 T T Y N Q K F K G K A T L T V D T S S S  
 301 ACAGCCAAG TGATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA TTTCTGTGA  
 TGTCGGTTGC AGTGAAGTC GTCCGACTGT AGACTACTGA GACGTCAAGT AAAGACACGT  
 78 T A N V H L S S L T S D D S A V Y F C A  
 361 AAGAGGACT ATGATACAA CGGCACTGG TTTTTCGATG TCTGGGGCG AGGACACAG  
 TCTCCCTGA TATCTATGTT GCCGCTGACC AAAAAGCTAC AGACCCCGG TCCCTGGTGC  
 98 R G D Y R Y N G D W F F D V W G A G T T  
 CDR #3  
 421 GTACCGTCT CCTCCGCTC CACCAAGGC CCATCGGTCT TCCCGCTGC ACCCTCTCC  
 CAGTGGCAGA GGAGGGGAG GTGGTTCCG GGTAGCCAGA AGGGGACCG TGGGAGGAG  
 118 V T V S S A S T K G P S V F P L A P S S  
 481 AAGAGCACT CTGGGGCAC AGCGGCCCTG GGTGCTG TCAAGGACTA CTTCGCCGA  
 TTCTCGTGA GACCCCGCTG TCGCCGGAC CCGACGACC AGTTCTGAT GAAGGGCTT  
 138 K S T S G G T A A L G C L V K D Y F P E  
 541 CCGTGAAGC TGTCTGGA CTCAGCGGC CTGACCAAGC GCGTGCACAC CTTCGCCGT  
 GGCACTGCC ACAGCACTT GAGTCCGCG GACTGGTCC CGACGCTGT GAAGGGCCGA  
 158 P V T V S W N S G A T T S G V H T F P A  
 601 GTCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGC TGACCGTGC CTCCAGCAGC  
 CAGGATGTA GGAGTCTGA GATGAGGAG TCGTCCGACC ACTGCGCAGG GAGGTGCTG  
 178 V T Q S S G L Y S T S S V V T V P S S S



661 TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTGAC  
 AACCCTGGG TCTGATGTA GACGTGCAC TTAGTGTTCG GGTGTTGTG GTTCACCTG  
 198 L G T Q T Y I C N V N H K P S N T K V D  
 721 AAGAAGTTG AGCCCAATC TTGTGACAAA ACTCACACAT GA (SEQ ID NO: 43)  
 TTCTTCAAC TCGGTTTAG AACACTGTTT TGAGTGTGA CT  
 218 K K V E P K S C D K T H T O (SEQ ID NO: 44)

FIG. 28B

FIG. 29

Variable Light Chain Domain

6G425  
F(ab)-1  
humkl

DIQTPTPLSPVSLDQASISCRSSQSLVHGIQNTYLTLMWYDQKPKGLIY  
DIQTGPSSSLASVGDRTITICFASKTI-----SKYLAWYDQKPKGAPKLLIY  
=====

L1  
+++++

6G425  
F(ab)-1  
humkl

YKSNRPFSGVDFDRFSDSGDFTLRIISRAVEADLGLVFCQSQSTHVPITFCAGTKLEKR  
YKSNRPFSGVDFDRFSDSGDFTLRIISRAVEADLGLVFCQSQSTHVPITFCAGTKLEKR  
YKSNRPFSGVDFDRFSDSGDFTLRIISRAVEADLGLVFCQSQSTHVPITFCAGTKLEKR  
=====

L2  
+++++

L3  
+++++

(SEQ ID NO: 45)  
(SEQ ID NO: 46)  
(SEQ ID NO: 47)

Variable Heavy Chain Domain

6G425  
F(ab)-1  
humIII

EIQDQSGPELTKPGASVKISCKASGYSPFSSHYMHVQSHGKSLMI  
EVLVESGGGLVQPGGSLRLSCAASGYSFSSHYMHVQAPGKGLEW  
EVLVESGGGLVQPGGSLRLSCAASGYSFSSHYMHVQAPGKGLEW  
=====

H1  
+++++

6G425  
F(ab)-1  
humIII

GYIDPSNGETTYNQKFKGKATLLTVDTSSSTAVHLSLTSDDSAVYFCAAARGDYRYNGDWFFDVWGAGT  
GYIDPSNGETTYNQKFKGKATLLTVDTSSSTAVHLSLTSDDSAVYFCAAARGDYRYNGDWFFDVWGAGT  
GMHPDSETRYYADSVKGRFTISRDNKNTLYLQHMNSLRAEDTAVYYCAARGIYFY-GTTFDYWGQGT  
=====

H2  
+++++

H3  
+++++

(SEQ ID NO: 48)  
(SEQ ID NO: 49)  
(SEQ ID NO: 50)

FIG. 30A

IC50~12nM

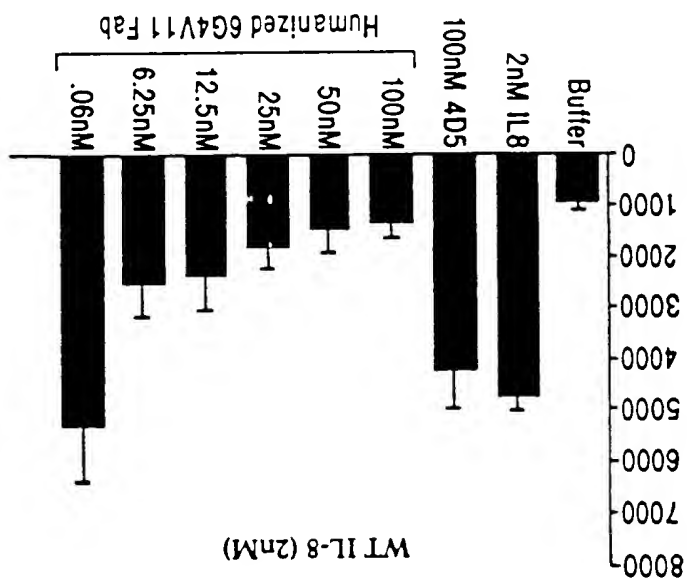


FIG. 30B

IC50~15nM

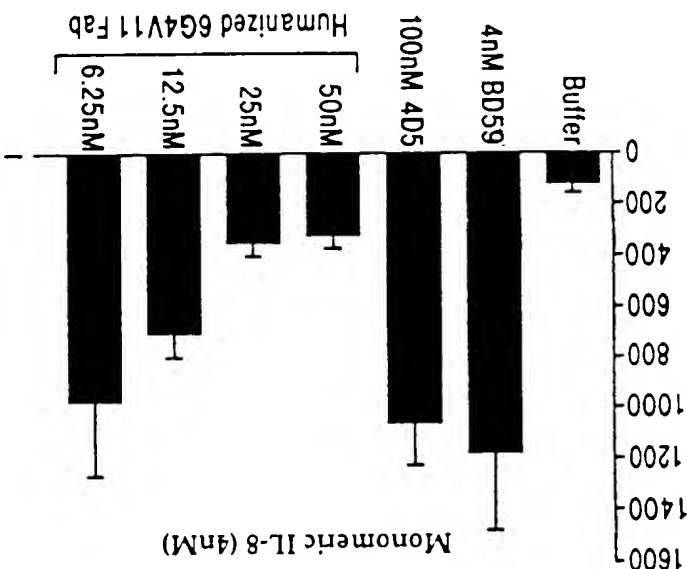
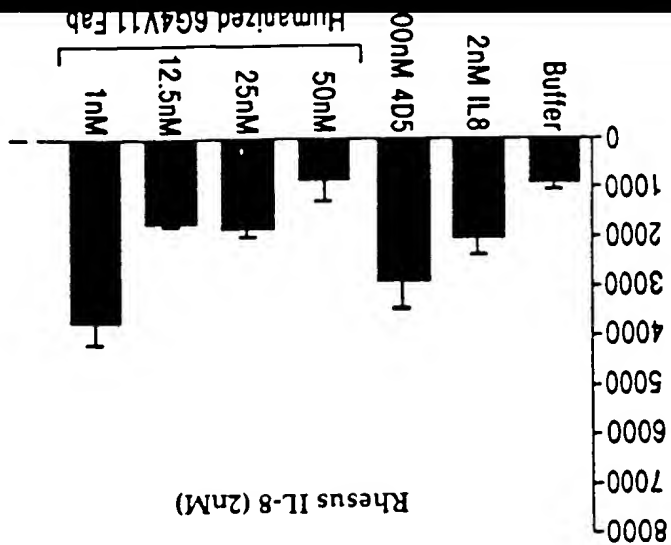


FIG. 30C

IC50~22nM



**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Light Chain**

MKKNIAFLLASMEVFSIATNAYADIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGNTY  
LHWYQQKPGKAPKLLIKVSNRFSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCSQST  
HVLPTFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN  
ALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
EC (See ID NO: 51)

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11 Heavy Chain**

MKKNIAFLLASMEVFSIATNAYAEVOLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH  
WVRQAPGKLEWVGVIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNLSLRAEDTAVYY  
CARGDYRYNGDWFEFDVWGQTLTVSSASTKGPVFPLAPSSKSTSGGTALGCLVKDYF  
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK  
VDKVEPKSCDKTHT (See ID NO: 52)

**Amino Acid Sequence of the peptide linker and M13 Phage Coat (gene-III)**

SGGSGSGDFDYEKMANANKGAMTENADENALQSDAKGLDSVATDYGAIDGFIGDVS  
GLANGNGATGDFAGSSNSQMAQVGDGDN SPLMNNFRQYLPSLPQSVCECRPFVFSAGKPY  
EFSIDCDKINLFRGVFAFLLYVATFMVVFSTFANILRNKES (See ID NO: 53)

**FIG. 31A**

1 ATGAAAAGA ATATCCGATT TCTTCTGCA TCTATGTTG TTTTCTAT TGCTACAAC  
-23 M K K N I A F L L A S M F V F S I A T N  
61 GCATACGCTG ATATCCAGAT GACCAGTCC CGAGCTCC TGTCGCCCTG TGTCGCCGAT  
-3 A Y A D I Q M T Q S P S S L S A S V G D

121 AGGCTACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TAACAGGTAT  
18 R V T I T C R S S Q S L V H G I G N T Y  
181 TTACACTGGT ATCAACAGAA ACCAGGAAA GCTCCGAAAC TACTGATTTA CAAGTATCC  
38 L H W Y Q Q K P G K A P K L L I Y K V S  
241 AATGATTCT CTGAGTCCC TTCTGCCTTC TCTGATCCG GTTCTGGAC GGATTACCT  
58 N R F S G V P S R F S G S G S G T D F T  
301 CTGACCATCA GCAGTCTGA GCCAAGAC TTCGAATT ATTACTGTTG ACAGATTAT  
78 L T I S S L Q P E D F A T Y Y C S Q S T

361 CATGTCCCG TCACGTTTG ACAGGTACC AAGTGGAGA TCAACGAAC TGTGCTGA  
98 H V P L T F G Q G T K V E I K R T V A A  
421 CCATCTGTCT TCATCTTCCC GCATCTGAT GAGCAATTGA AATCTGGAAC TGTCTGT  
118 P S V F I F P P S D E Q L K S G T A S V  
481 GTGTCCCTGC TGAATACTT CTATCCAGA GAGGCCAAG TACAGTGAA GTTGATAAC  
138 V C L T N N F Y P R E A K V Q W K V D N  
541 GCCCTCCAAT CCGTAACTC CCAGGAGAT GTACAGAGC AGCAGACA GGACAGAC  
158 A L Q S G N S Q E S V T E Q D S K D S T

601 TACAGCTCA GCAGCACCT GACGCTGAGC AAAGCAAGT ACAGAAACA CAAGTCTAC  
178 Y S L S S T L T L S K A D Y E K H K V Y  
661 GCCTGCGAAG TCACCCATCA GGGCTGAGC TCGCCCGTCA CAAGAAGCTT CAACAAGGGA  
198 A C E V T H Q G L S S P V T K S F N R G  
721 GAGTGTAAAG CTGATCTCTT ACCCGGAGC CATCGTGGCC CTAGTACGA ACTAGTCTGA

218 E C O (56 10 10:51)  
CTCACAATTG GACTAGGAGA TGCGGCCCTG GTAGCACCGG GATCATGCGT TGATCAGCAT

FIG. 31B

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Light Chain**

MKKNIAFLASMEVFSIATNAYADIQMTQSPSSLSASVGDRVITTCRSSQSLVHGIGNTY  
LHWYQQKPGKAPKLLIKVSNRFSGVPSRFSGSGGTDFLTLTSSLOPEDFATYYCSQST  
HVLTFEGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDN  
ALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
EC (SEQ ID NO: 51)

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V19 Heavy Chain**

MKKNIAFLLASMEVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGYSFSSHYMH  
WVKQAPGKGLEWVGVIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY  
CARGDYRYNGDWFEDVWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTALGCLVKDYF  
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTK  
VDKKEPKSCDKTHT (SEQ ID NO: 55)

**FIG. 31C**

FIG. 32



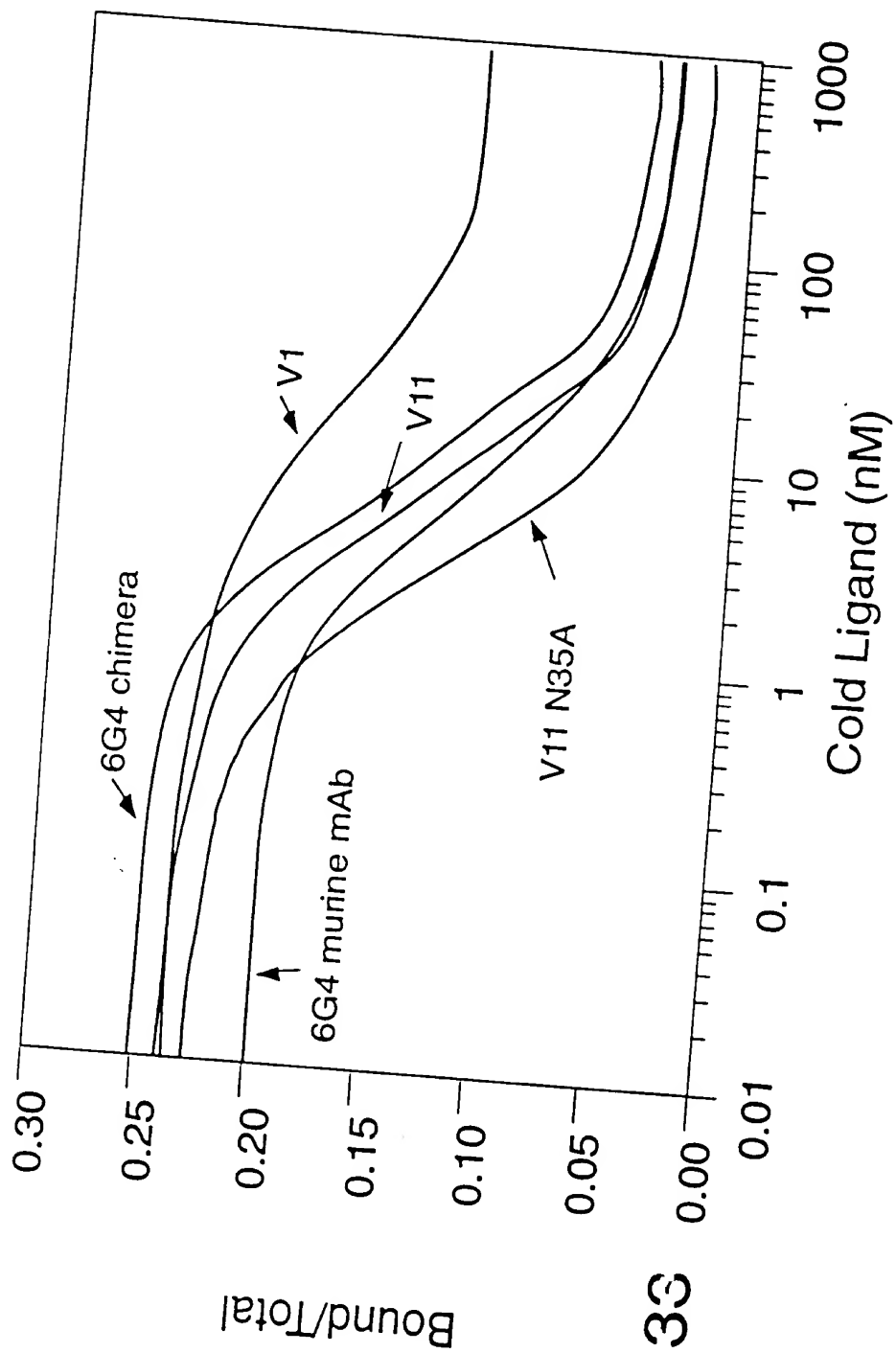
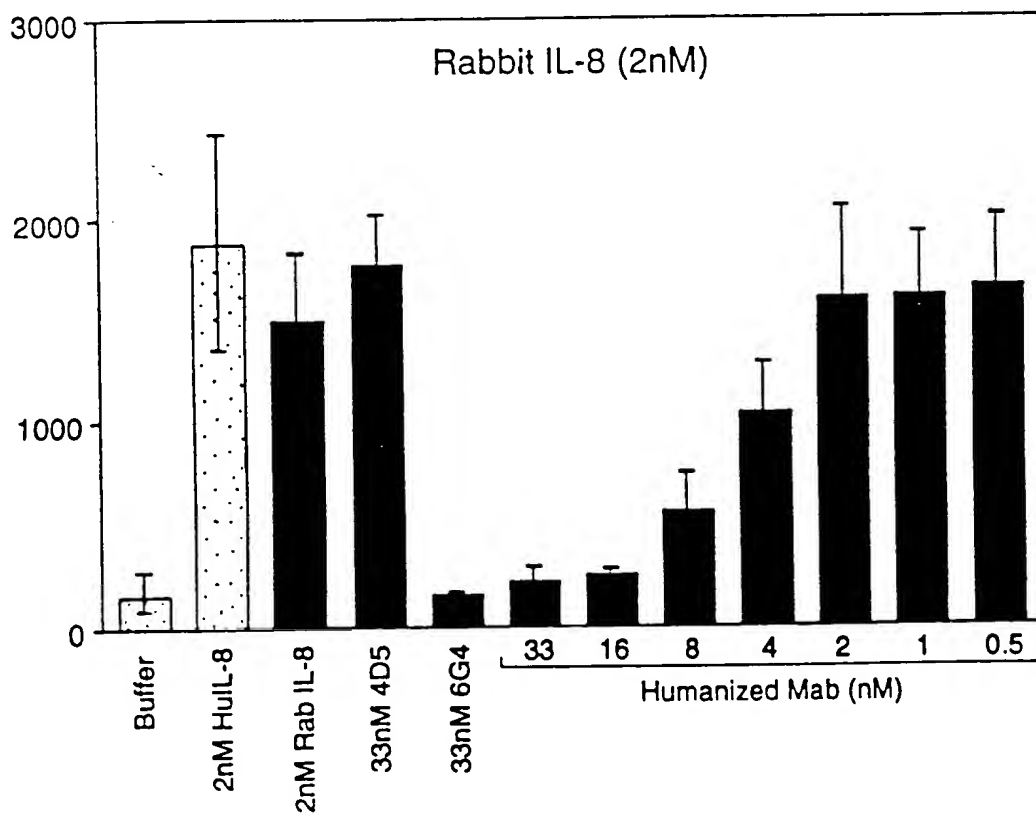
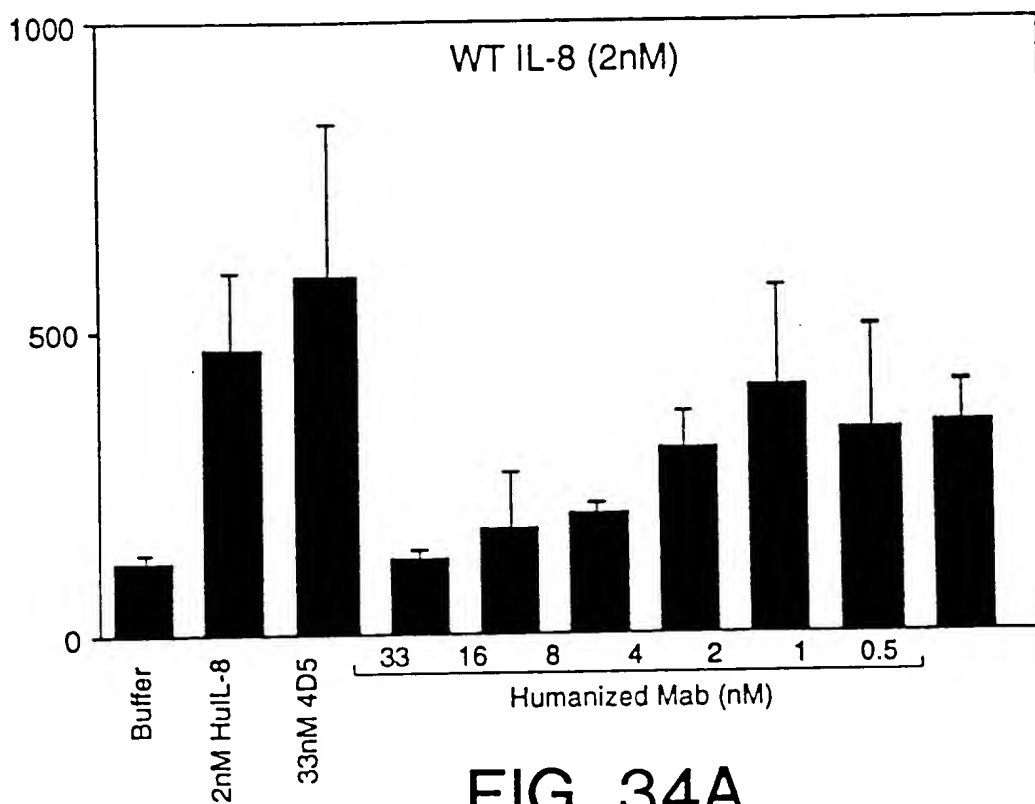


FIG. 33





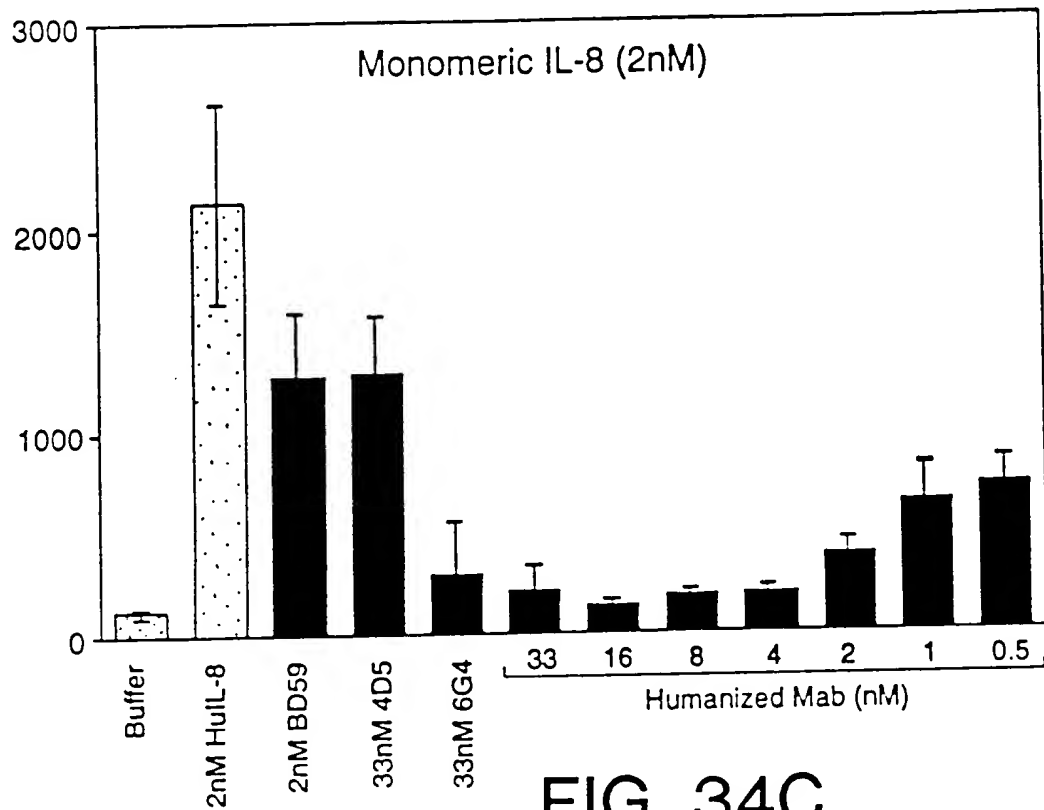


FIG. 34C

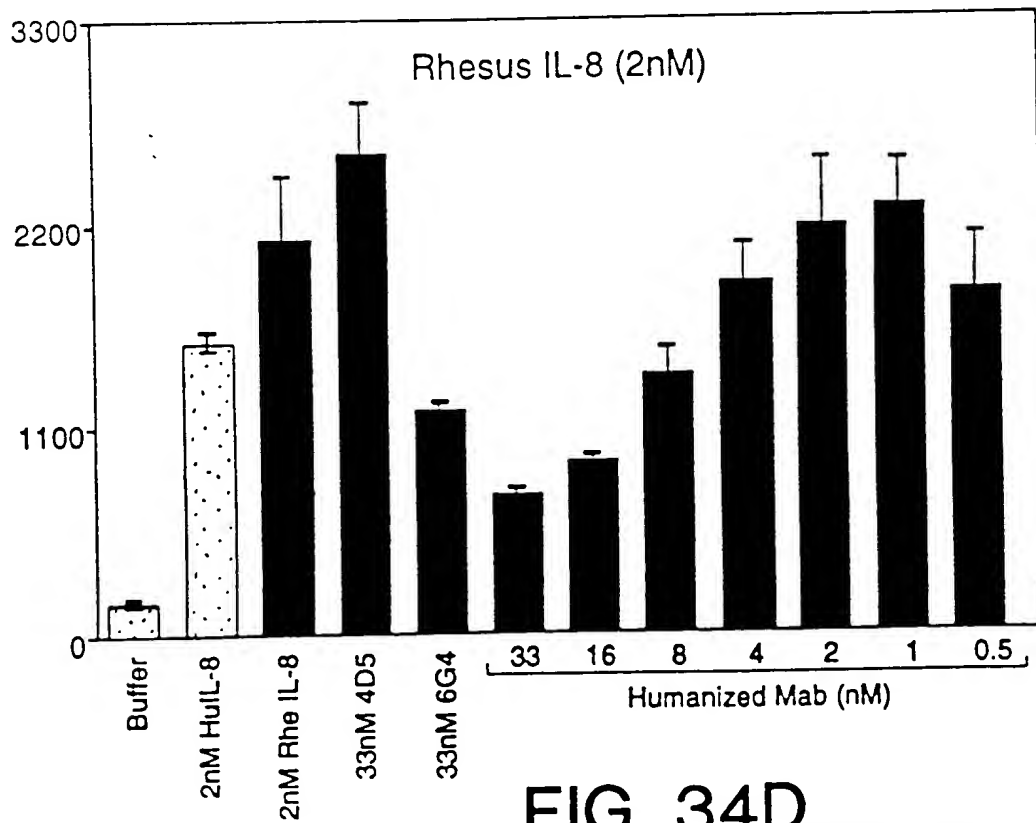


FIG. 34D

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Light Chain**

MKKNIAFLASMFVFSIATNAYADIQMTQSPSSLSASVGDRTTITCRSSQSLVHGIGATY  
LHWYQQKPGKAPKLLIYKVSNRFSGVPSRFSGSGGTDFTLTISSLQPEDFATYYCSQST  
HVPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLLNNFYPREAKVQWKVDN  
ALQSGNSQESVTEQDSKDSYSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
EC (SEQ ID NO: 56)

**Amino Acid Sequence of the humanized anti-IL-8 6G4.2.5V11N35A Heavy Chain**

MKKNIAFLASMFVFSIATNAYAEVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMH  
WVRQAPGKGLEWVGYYIDPSNGETTYNQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYY  
CARGDYRYNGDWFFDVWGQGLTVTVSSASTKGPVFFPLAPSSKSTSGGTAALGCLVKDYF  
PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHHKPSNTK  
VDKKVEPKSCDKTHT (SEQ ID NO: 57)

**Amino Acid Sequence of the putative Pepsin Cleavage Site and GCN4 Leucine Zipper**

CPPCPAPELLGGRMKQLEDKVEELL<sup>52</sup>SKNYHLENEVARLKKLVGER (SEQ ID NO: 57)

**FIG. 35**

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCG TTTTCTCTAT TGCTACAAAC  
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCGCCCTC TGTGGGCGAT  
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA  
 -3 A Y A D I Q M T Q S P S S L S A S V G D  
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGCTACGTAT  
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACGATGCATA  
 18 R V T I T C R S S O S L V H G I G A T Y  
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC  
 AATGTGACCA TAGTTGTCTT TGGTCCTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG  
 38 L H W Y Q Q K P G K A P K L L I Y K V S  
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT  
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA  
 58 N R F S G V P S R F S G S G S G T D F T  
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT  
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA  
 78 L T I S S L Q P E D F A T Y Y C S O S T  
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA  
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT  
 98 H V P L T F G Q G T K V E I K R T V A A  
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT  
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA  
 118 P S V F I F P P S D E Q L K S G T A S V  
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC  
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG  
 138 V C L L N N F Y P R E A K V Q W K V D N  
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC  
 CGGGAGGTTA GCCCATTGAG GGTCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTT  
 158 A L Q S G N S Q E S V T E Q D S K D S T  
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC  
 ATGTGCGAGT CGTCGTGGGA CTGCGACTCG TTTCTGTCTGA TGCTCTTTGT GTTTCAGATG  
 178 Y S L S S T L T L S K A D Y E K H K V Y  
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
 CGGACGCTTC AGTGGGTAGT CCCGACTCG AGCGGGCAGT GTTCTCGAA GTTGTCCCTT  
 198 A C E V T H Q G L S S P V T K S F N R G  
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA (SEQ ID NO: 58)  
 CTCACAATTC GACTAGGAGA TGCGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT  
 218 E C O (SEQ ID NO: 56)

FIG. 36

781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCTTGCA  
TTTTCCCATG GATCTCCAAC TCCACTAAAA TACTTTTTCT TATAGCGTAA AGAAGAACGT  
-1 M K K N I A F L L A

841 TCTATGTTTCG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTCAGCT AGTGCAGTCT  
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA  
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GCGGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC  
CGGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG  
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG  
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCTC GGACCTTACC  
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGATATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT  
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA  
48 V G Y I D P S N G E T T Y N O K F K G R

1081 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT  
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA  
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG  
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCCTAA TAGCGATGTT ACCACTGACC  
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC  
AAGAAGCTGC AGACCCCACT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG  
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGACAC AGCGGGCCCTG  
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCGTG TCGCCGGGAC  
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC  
CCGACGGACC AGTTCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG  
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTACTCCCTC  
GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCCTGA GATGAGGGAG  
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG  
TCGTGCGACC ACTGGCACGG GAGGTCGTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC  
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA  
TTAGTGTTTCG GGTGCTTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT  
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTG CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA  
TGAGTGTTGA CGGGCGGCAC GGGTCGTGGT CTTGACGACC CGCCGGCGTA CTTTGTGAT  
228 T H T C P P C P A P E L L G G R M K Q L

FIG. 37A

1621 GAGGACAAGG TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA  
CTCCTGTTCC AGCTTCTCGA TGAGAGGTTC TTGATGGTGG ATCTCTTACT TCACCGTTCT  
248 E D K V E E L L S K N Y H L E N E V A R

1681 CTCAAAAAGC TTGTCGGGGA GCGCTAA (SEQ ID NO: 59)  
GAGTTTTTCG AACAGCCCCT CGCGATT  
268 L K K L V G E R O (SEQ ID NO: 60)

FIG. 37B

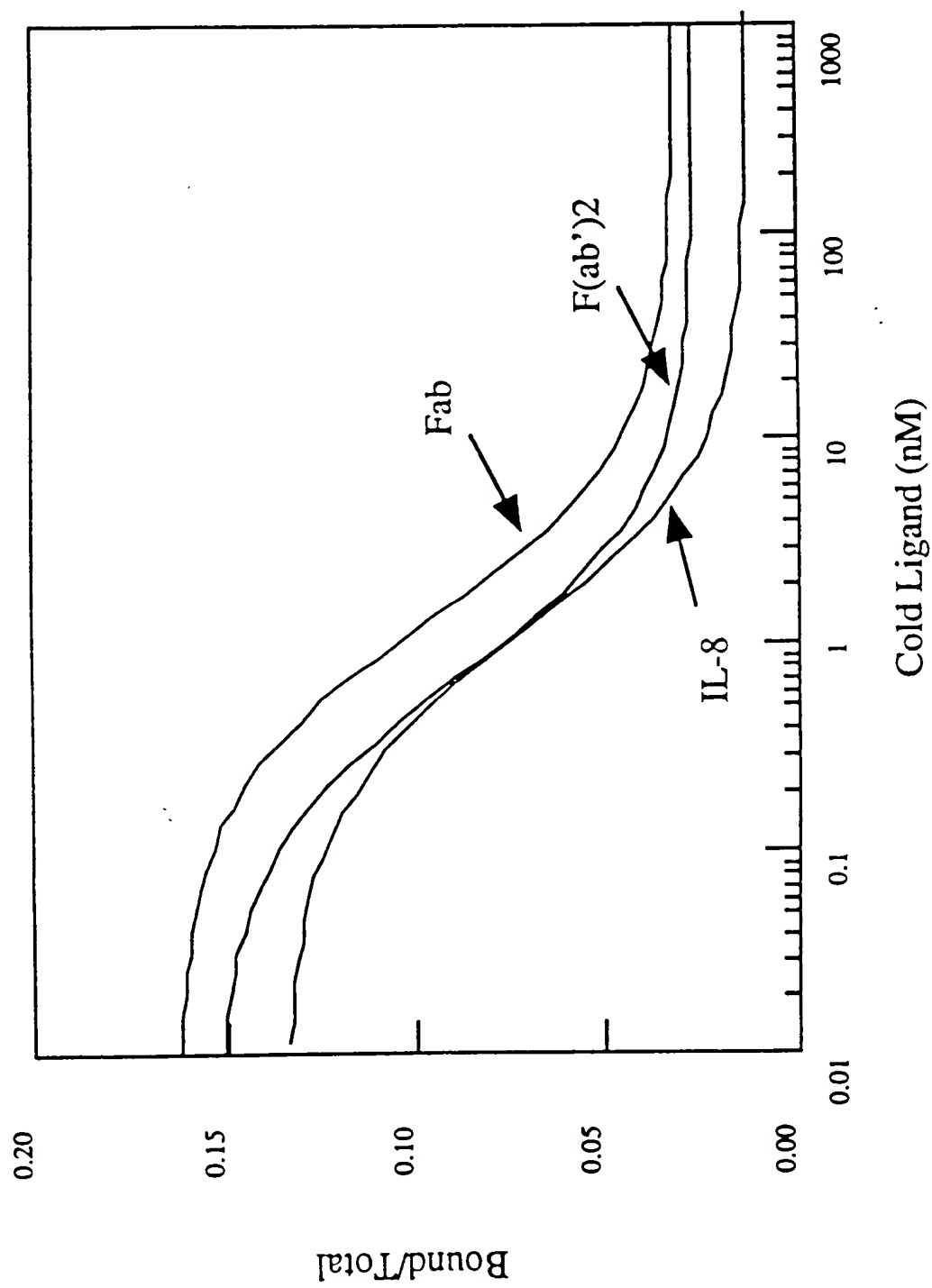


FIG. 38

FIG. 39

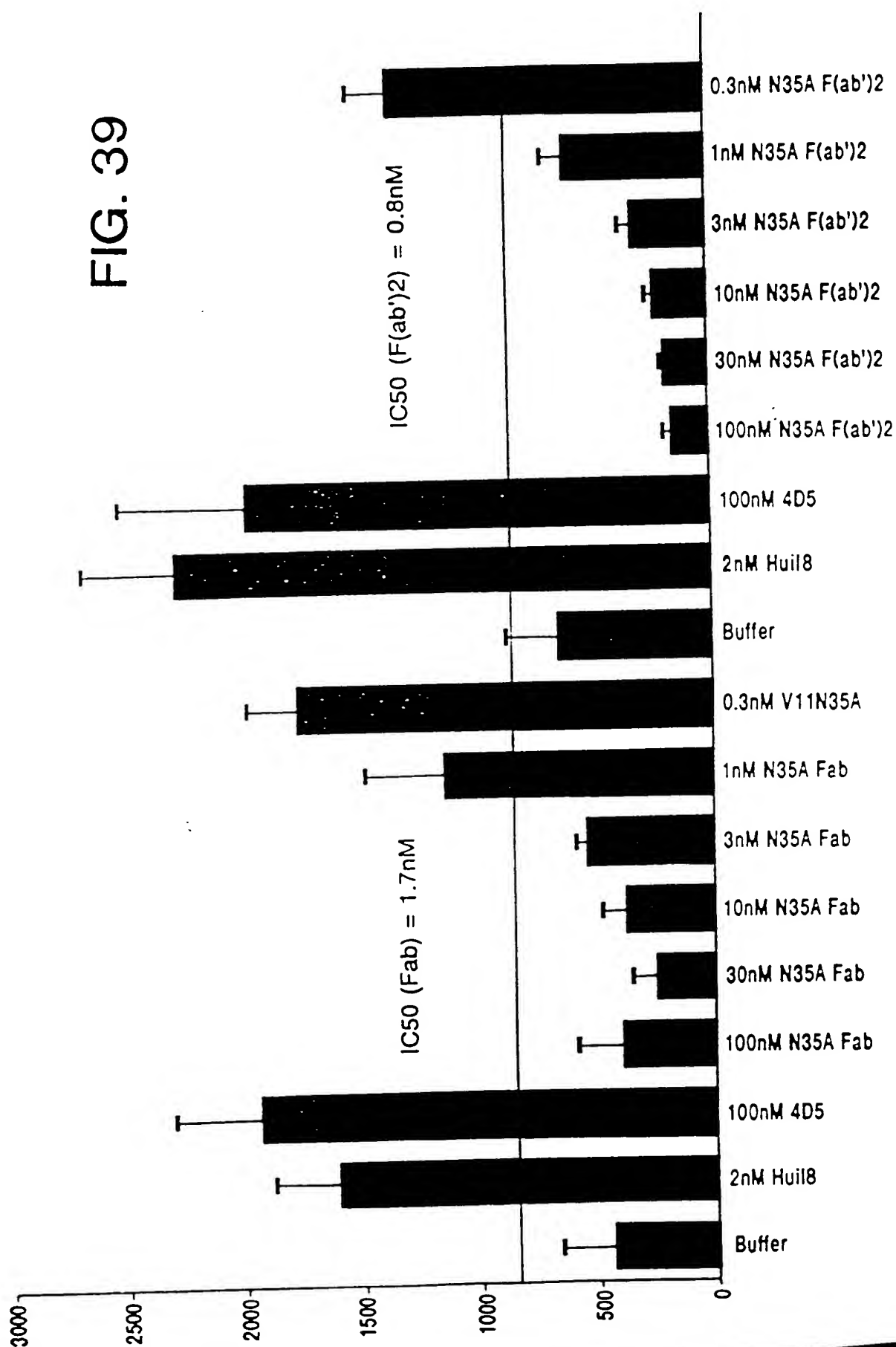
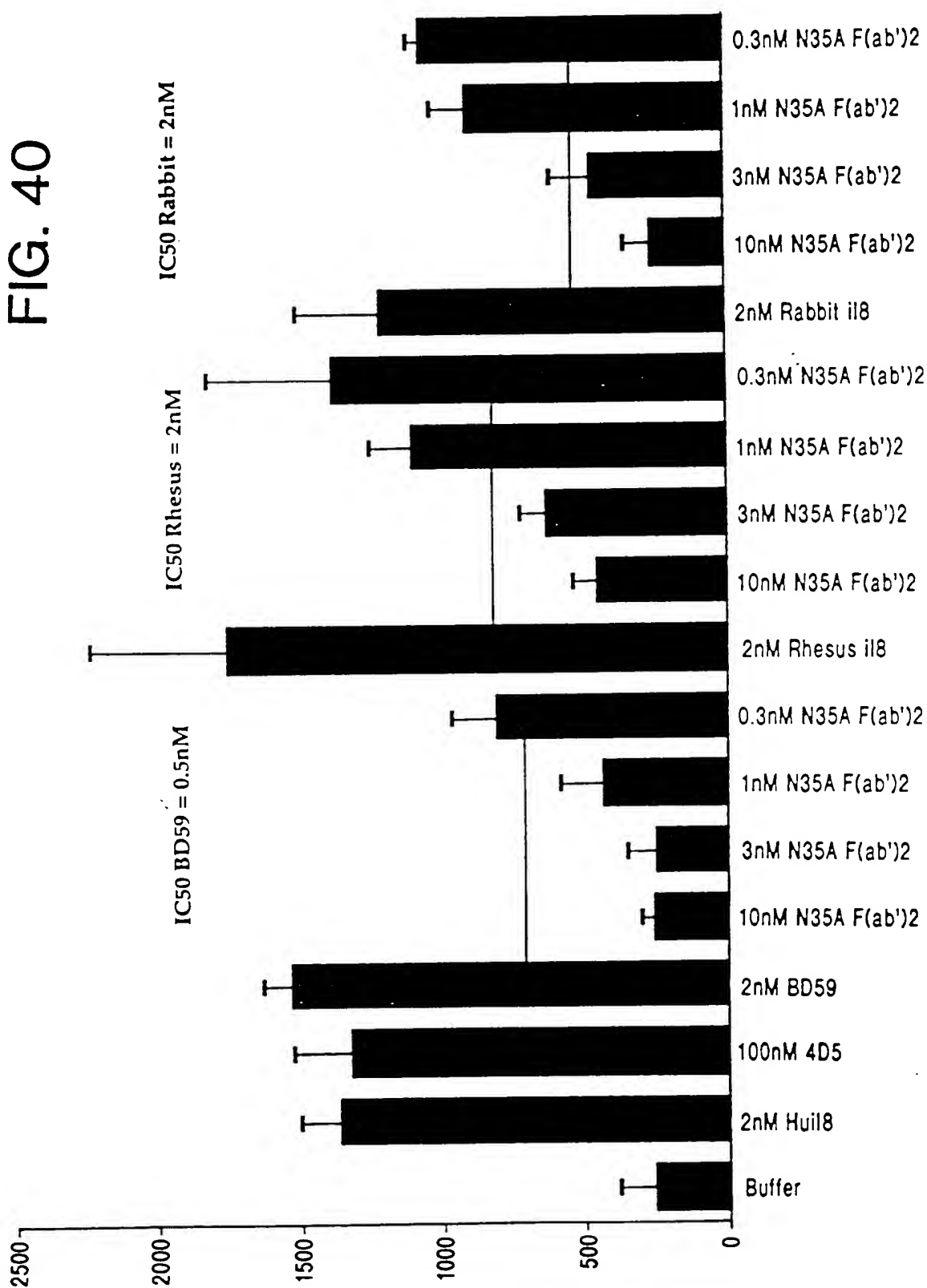




FIG. 40



ecoRI pflMI  
apoI bslI  
1 GAATTCAACT TCTCCATACT TTGGATAAGG AATACAGAC ATGAAMAATC TCATTGCTGA GTTGTATTAT AGCTTGCCC AAAAGAAGA AGAGTCGAAT CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTG TACTTTTTAG AGTACGACT CAACAATAMA TTCGAACGGG TTTTCTTCT TCTCAGCTTA

alul pleI  
hindIII taqI  
tru9I mboII carI/ksp632I  
mseI cac8I mboII hinfi  
TTCGAACGGG TTTTCTTCT TCTCAGCTTA

bspMI  
hinPI  
hhaI/cfoI  
mstI aluI  
avlII/fspI hindIII  
101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG CTTGACACAC GCGTCCATCT TCGMAACCTC TAATAGCAGT GACGTTATAC AGCGTTATAC CCGGTTTAC TGGTTGTCGC CAACTAACCTA GTCCATCTCC

sau3AI  
mboI/ndeII[dam-]  
dpnI[dam+]  
dpnII[dam-] aciI  
hinPI hhaI/cfoI nspBII bclI[dam-] mnII  
thaI fnuDII/mvni  
fnu4HI bsoFI bbvI maeII  
fnu4HI bstUI snaBI bsoFI bsh1236I  
bbvI hinPI bsaAI aluI hhaI/cfoI  
maeII foki sfaNI  
mnII

rsai  
hinPI  
hhaI/cfoI mnII  
haeII csp6I  
201 GGCGGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGNAGTTA TTGAAGCATC CTCGTACGTA CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTNAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

alul  
astI sacI  
hgiJII  
hgiAI/aspHI  
ec1136II  
ecoRI bspl286  
tmai bsiHKAI  
maei bmyI  
bfai taqI  
apuI apoI banII  
mscI mscI  
tru9I mscl  
maeIII apol banII  
TTTGAACCTA GAATTCGAGC  
TTTGAACCTA TTTTATGCTA  
AAAATTACAT AAACATTGAT CTTAAGCTCG

haeIII/pali  
mcRI  
eagI/xmaIII/ec1XI  
caeI cfri  
bsiEI ahdI/eaml105I  
maeIII bsmAI  
aluI  
pvuII  
nspBII  
tru9I mvuII  
mseI  
101 AAAAGTTAAT CTTTTCACCA GCTGTCATAA AGTTGTACAG GCCAGACTT ATAGTCGCTT TGTTTTTATT TTTTAACTA TTTGAACCTA GAATTCGAGC TTTTCAATTA GAAAGTTGT CGACAGTATT TCAACAGTGC CCGCTCTGAA TATCAGCGAA ACANAAATMA AAAATTACAT AAACATTGAT CTTAAGCTCG

FIG. 41A

[illegible]

601	GGTATAGGTG	CTACGTATTT	ACACTGGTAT	CAACAGAAAC	CAGGAAAGC	TCCGAAACTA	CTGATTACAA	AAGTATCCAA	TCGATTCTCT	GGAGTCCCTT
	CCATATCCAC	GATGCATATA	TGTGCTTTTG	GTCCTTTTCG	AGGCTTTGAT	GACTAATGT	TTCATAGGTT	AGCTAAGAGA	CCTCAGGGAA	
32	G I G A	T Y L H	W Y Q Q	K P G K	A P K L	L I Y K	V S N R	F S G V	P S	

66	R F S G	S G S G	T D F T	L T I S	S L Q P	E D F A	T Y Y C	S S Q S	T H
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701	CTCGCTTCTC	TGGATCCGGT	TCTGGGACGG	ATTCACTCT	GACCATCAGC	AGTCTGCAGC	CAGAGACTT	CGCAACTTAT	TACTGTTTAC	AGAGTACTCA
	GAGCGAAGAG	ACCTAGGCCA	AGACCTTGCC	TAAAGTGAGA	CTGGTAGTCG	TCAGACGTCG	GTCTTCTGAA	GCGTTGAATA	ATGACAAGTG	TCTCATGAGT

9	V P L T	F G Q G	T K V E	I K R T	V A A P	S V F I	F P P S	D E Q L	K
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1	TCCTCCGCTC	ACGTTTGAC	AGGTACCAA	GGTGGAGATC	AAACGNACTG	TGGCTGCACC	ATCTGTCTTC	ATCTTCCCGC	CATCTGATGA	GCAGTTGAAA
	ACAGGGCGAG	TGCAAACTG	TCCCATGGTT	CCACCTCTAG	TTTGCTTGAC	ACCGACGTCG	TAGACAGAG	TAGAAGGGCG	GTAGACTACT	CGTCAACTTT

FIG. 41C

#cIFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bsaJI  
 maeIII apyI[dcM+]

xmnI  
 asp700  
 cac8I  
 asp700  
 xmnI  
 haeIII/palI  
 haeI  
 isaI  
 mnlI  
 csp6I  
 maeIII apyI[dcM+]

901 TCTGGACTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCACAGAGA GCCCAAGTA CAGTGGAGG TGGATAAGC CCTCCAATCG GGTAACTCCC  
 AGACCTTGAC GAAGACNACA CACGGACGAC TTATTGAAGA TAGGGTCTCT CCGGTTTCAT GTCACCTTCC ACCTATTGCG GGAGGTTAGC CCATTGAGGG

132 S G T A S V V C L L N N F Y P R E A K V Q W K V D N A L Q S G N S Q

fnu4HI  
 bsoFI  
 ddeI  
 mnlI  
 bbvI  
 hgaI  
 ddeI  
 cellI/espi  
 blpI/bpull02I  
 accI  
 cac8I

maeIII  
 scfI  
 mnlI  
 bbvI  
 hgaI  
 ddeI  
 cellI/espi  
 blpI/bpull02I  
 accI  
 cac8I

01 AGGAGAGTGT CACAGAGCAG GACAGCMAGG ACAGCACCTA CAGCCTCAGC AGCACCTCTGA CGCTGAGCA AGCAGACTAC GAGAAACACA AAGTCTACGC  
 TCCCTCACA GTGTCTCGTC CTGTCTGTC TGTCTGTC GTCTGTCGTGTC TGTCTGTCGTGTC TGTCTGTCGTGTC TGTCTGTCGTGTC TGTCTGTCGTGTC

56 E S V T E Q D S K D S T Y S L S S T L T L S K A D Y E K H K V Y A

cac8I  
 aluI  
 bstI  
 sacI  
 hgiJII  
 hgiAI/aspHI  
 ecl136II  
 bsp1286  
 bsiHKAI  
 bmyI  
 haeIII/palI  
 sau96I  
 banII  
 asuI  
 ddeI  
 hphI  
 maeIII  
 alwNI[dcM-]  
 CTGGGAAGTC ACCCATCAGC GCCTGAGCTC GCCCGTCACA AAGAGCTTCA ACAGGGGAGA GTGTTAAGCT GATCTCTAC GCCGACGCA TCGTGGCCCT  
 GACGCTTCAG TGGGTAGTC CGGACTCGAG CGGGCAGTGT TTCTCGAAGT TGTCCTCTCT CACAAATCGA CTAGGAGATG CGGCCTGCGT AGCACCGGGA  
 C E V T H Q G L S S P P V T K S F N R G E C O (SEE NO: 56)

mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 aluI  
 dpnI[dam+] hgaI  
 tru9I  
 dpnII[dam-] mspI  
 mseI  
 alwI[dam-] hpaII  
 sfaNI  
 asuI  
 haeIII/palI

rmaI  
 maeI  
 bfaI  
 sau96I

FIG. 41D

[illegible]

scrFI  
ncII  
mspI  
hpaII  
dsav  
cauII  
bsII  
xmaI/pspAI  
smaI  
scrFI  
ncII  
dsav  
cauII  
bsII

scrFI  
mvaI  
ecorII

FIG. 41E

1401 CTTCTCCAGT CACTATATGC ACTGGGTCCG TCAGGCCCGG GGTAAAGGCC TGGMATGGGT TGGATATATT GATCCTTCCA ATGGTGAAC TACGTATAAT  
GAAGAGCTCA GTGATATACG TGACCCAGGC AGTCCGGGCG CCATTCCCGG ACCTTACCCA ACCTATATAA CTAGGAAGGT TACCACCTTG ATGCATATTA  
29 F S S H Y M H W V R Q A P G K G L E W V G Y I D P S N G E T T Y N

301 CAAAGTTCA AGGCGCGTTT CACTTTATCT CGCGACNACT CCNAAACAC AGCATACTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT  
GTTTTCAGT TCCCGGCAAA GTGAATAGA CGCTGTGTA GGTTTTGTG TCGTATGGAC GTCTACTGT CGGACGCACG ACTCCTGTGA CGGCAGATAA  
62 Q K F K G R F T L S R D N S K N T A Y L Q M N S L R A E D T A V Y Y

63 C A R G D Y R Y N G D W F F D V W G Q G T L V T V S S A S T K G P  
seq right is from p6G425chlm2.fab2

FIG. 41F

[illegible]

FIG. 41G



2001	TCACACATGC	CGCCGTGCC	CAGCACCAGA	ACTGCTGGG	GGCCGATGA	AACAGCTAGA	GGACAAGGTC	GAAGAGCTAC	TCTCCAAGAA	CTACCACCTA
229	H T C P P C P A P E L L G G R M K Q L E D K V E E L L S K N Y H L									
	~junction between antibody and leucine zipper									

2101	GAGAATGAAG	TGGCAAGACT	CAAAAGCTT	GTCCGGGAGC	GCTAACCATG	CGACGGCCCT	AGAGTCCCTA	ACGCTCGGTT	GCCGCCGGGC	GTTTTTTATT
262	E N E V A R L K K L V G E R O (56419 60)									

2201	CTTAACCTCAT	GTTTGACAGC	TTATCATCGA	TAAGCTTTAA	TGCGGTAGTT	TATCACAGTT	AAATTGCTAA	CGCAGTCAGG	CACCGTGTAT	GAATCTAAC
	CAATTGAGTA	CAAACTGTGC	AATAGTAGCT	ATTGGAATT	ACGCCATCAA	ATAGTGTCAA	TTTAACGATT	CGGTACAGTCC	GTGGCACATA	CTTTAGATTG

FIG. 41H

21 sfANI  
 scrFI sau96I haeIII/palI  
 mvaI scrFI  
 ecorII nciI  
 dsav rsal mspI mnlI  
 bstNI csp6I hpalI  
 nlaIV mspI dsav bsII ecorV  
 mnII hglCI hpalI cauII  
 bsajI hphI apyI[dcmt+] cfrI0I/bsrFI asuI acII  
 hlnPI hhaI/cfoI foki bani maeIII foki scfI  
 hhaI/cfoI TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTCGGGGAT ATCGTCCATT  
 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG GACATCCGTA TCCGNACCAA TACGGCCATG ACGGCCCGGA GAAGGCCCTA TAGCAGGTAA  
 TTACGGGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC

hinPI  
 hhaI/cfoI  
 imaI  
 maeI  
 nheI  
 fnu4HI haeII  
 bsoFI eco47III  
 bbvI bfaI  
 maeIII  
 sfANI bsrI cac8I cac8I  
 TATGGCGTGC TGCTAGCGCT ATATGCGTTG ATGCAATTC TATGGCGACC CGTTCTCGGA GCACGTGTCG ACCGCTTTGG  
 CGGTCAGTG ATACCGCAGG ACGATCGCGA TATACGCAAC TAGCTTAAAG ATACGGCTGG GCAAGAGCCT CGTGACAGGC TGCCGAAACC  
 GGCTGTCTGA

acII  
 fnu4HI  
 bsoFI  
 acII bsrI cac8I  
 GTCTGCTCG CTTCGCTACT TGGAGCCACT ATCGACTACG CGATCATGCG GACCACACCC GTCTGTGGA TCCTCTACGC CGGACGCATC  
 CCGCGGCCCA CAGGCGATGA ACCTCGGTGA TAGCTGATGC GCTAGTACCG CTGGTGTGG CAGGACACCT AGGAGATCGG GCCTGCGTAG  
 GGCGGCGGGT

acII  
 fnu4HI  
 bsoFI  
 hinPI  
 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
 bmyI  
 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
 mcrI  
 bsiEI  
 cfrI  
 fnu4HI  
 bsoFI  
 haeIII/palI  
 acII  
 eacI  
 bmyI  
 cfrI  
 mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
 bamHI  
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 alwI[dam-]  
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 bsiEI  
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 bsoFI  
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 alwI[dam-]  
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 avIII/fspI  
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 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
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 bsiEI  
 cfrI  
 fnu4HI  
 bsoFI  
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 bmyI  
 cfrI  
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 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
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 bstVI/xhoII  
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 mspI  
 alwI[dam-]  
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 hglAI  
 hhaI/cfoI  
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 avIII/fspI  
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 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
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 bsiEI  
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 fnu4HI  
 bsoFI  
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 cfrI  
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 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
 bamHI  
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 alwI[dam-]  
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 sfANI  
 hglAI  
 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
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 cfrI  
 fnu4HI  
 bsoFI  
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 mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
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 alwI[dam-]  
 hpalI  
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 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
 bmyI  
 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
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 bsiEI  
 cfrI  
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 bmyI  
 cfrI  
 mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
 bamHI  
 mspI  
 alwI[dam-]  
 hpalI  
 sfANI  
 hglAI  
 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
 bmyI  
 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
 mcrI  
 bsiEI  
 cfrI  
 fnu4HI  
 bsoFI  
 haeIII/palI  
 acII  
 eacI  
 bmyI  
 cfrI  
 mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
 bamHI  
 mspI  
 alwI[dam-]  
 hpalI  
 sfANI  
 hglAI  
 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
 bmyI  
 hglAI/aspHI  
 bsp1286  
 bsiHKAI  
 mcrI  
 bsiEI  
 cfrI  
 fnu4HI  
 bsoFI  
 haeIII/palI  
 acII  
 eacI  
 bmyI  
 cfrI  
 mnlI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-]  
 nlaIV  
 bstVI/xhoII  
 bamHI  
 mspI  
 alwI[dam-]  
 hpalI  
 sfANI  
 hglAI  
 hhaI/cfoI  
 mgtI bsII  
 avIII/fspI  
 bmyI  
 hglAI/aspHI  
 bsp1286  
 bsiHKAI

FIG. 41I

hinPI  
 hhaI/cfoI  
 nlaIV  
 nari  
 kasi  
 hinII/acyI  
 hgiCI  
 haeII  
 mspI  
 cfr10I/bsrFI bani  
 cac8I sgrAI  
 haeIII/pali hpaII  
 eaeI hphI ahaII/bsaHI  
 cfrI sfaNI cfr10I/bsrFI acII cac8I  
 501 GTGGCCGGCA TCACCGGGCG CACAGGTGCG GTTGCTGGCG CCTATATCGG CGACATCACCC GATGGGGAAG ATCGGGCTCG CCACCTTCGGG CTCATGAGCG  
 CACCGGCCGT AGTGGCCGCG GTGTCCACGC CAACGACCCGC GGATATAGCG GCTGTAGTGG CTACCCCTTC TAGCCCGAGC GGTGAAGCCC GAGTACTCGC

hinPI  
 hhaI/cfoI  
 nlaIV  
 nari  
 kasi  
 hinII/acyI  
 hgiCI  
 haeII  
 bani  
 ahaII/bsaHI  
 cac8I  
 hphI  
 hgiJII  
 bsp1286  
 bmyI  
 banII  
 sau3AI cac8I  
 mboI/ndeII[dam-]  
 dpmI[dam+]  
 dpmII[dam-]  
 mboII[dam-]  
 hphI  
 hgiJII  
 bsp1286  
 bmyI  
 banII  
 rcaI  
 hinPI  
 haeII  
 eoa47III  
 bmyI bspHI hhaI/cfoI  
 banII nlaIII  
 mboII[dam-]  
 CCACCTTCGGG CTCATGAGCG  
 GGTGAAGCCC GAGTACTCGC

scrFI  
 nciI  
 mspI  
 hpaII  
 dsal dsav  
 bsII cauII  
 sau96I haeIII/pali  
 nlaIV eaeI  
 haeIII/pali  
 asuI bsaJI bsaJI  
 ecoO109I/draII  
 cac8I bsII cfrI bsmFI  
 1 CTTGTTTCGG CGTGGCTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG GCGGCATCTT CCTTGCACGC ACCATTCTTT GCGCGCCGCG TGTCTCAACGG  
 GAACAAAGCC GCACCCATAC CACCGTCCGG GGCACCGGCC CCCTGACAAAC CCGCGGTAGA GGAACGTGCG TGTAAGGAA CCGCGCCGCG ACCAGTTGCC

fnu4HI  
 bsoFI econI  
 bsII bsvI bsII  
 mnlI bsII bsrI bsvI  
 CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG  
 GGAGTTGGAT GATGACCCGA CGAAGGATTA CGTCCTCAGC GTATTCCCTC TCGCAGCAGG CTACGGGNAAC TCTCGGAAGT TGGGTCAAGT GAGGAAGGCC

fnu4HI  
 bsoFI hgiAI/aspHI  
 acII bsp1286  
 fnu4HI bsiHKAI  
 bsoFI bmyI  
 bsII acII acII  
 bslI acII acII  
 haeIII/pali  
 mspI  
 hpaII  
 bsaWI  
 bsrI aluI bsII

FIG. 41J

acII  
 thai  
 fnuDII/mvni  
 bstUI  
 bsh1236I  
 hinPI  
 hhai/cfoI  
 acII  
 fnu4HI  
 bsoFI  
 mboII  
 bpuAI  
 bbsI  
 nlaIII  
 bani hpaII hhai/cfoI  
 mnlI  
 2901 TGGGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT CATGCACTC GTAGGACAGG TGCCGGCAGC GCTCTGGTC ATTTTCGGCG  
 ACCGCGGCC CGTACTGATA GCAGCGCGGT GAATACTGAC AGAAGAATA GTACCTTGAG CATCCTGTCC ACGGCCGTCC CGAGACCCAG TAAAGCCGC  
 acII  
 sau96I  
 avaiI  
 asuI  
 bpmI/gsuI[dcM-] dpmII[dam-]  
 bpml/gsuI[dcM-] dpmII[dam-]  
 3001 ACGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCCTGTC GCTTGGGTA TTCGGGAATCT TGCACGCCCT CGCTCAAGCC TCGTCACTG GTCCCGCCAC  
 TCCTGGCGAA AGCGACCTCG CGCTGCTACT AGCCGGACAG CGAACGCCAT AAGCCTTAGA ACGTGCGGA CGAGATTCCG AAGCAGTGAC CAGGCGGTG  
 mcrI  
 eagI/xmaIII/eclXI  
 eaeI  
 cfrI  
 bsiEI  
 fnu4HI  
 cfr10I/bsrFI  
 haeIII/pali  
 haeI  
 cac8I  
 bgII nlaIII haeIII/pali  
 GCGCGCATG GCGGCCGACG CGCTGGGCTA CGTCTTGCTG GCGTTCGCA CGCGAGGCTG GATGCCCTC  
 GTTTGAAG CCGCTCTTCG TCCGGTAATA GCGCGGTAC GCGCGGCTG CCGACCCGAT GCAGACGAC CGCAAGCGCT GCGCTCCGAC CTACCGGAAG  
 maeII  
 psp1406I  
 CAAACGTTTC GCGCAGAAGC AGGCCATTAT  
 fnu4HI  
 mspi  
 hinPI  
 hhai/cfoI  
 bsiEI  
 fnu4HI  
 fnuDII/mvni  
 bstUI  
 bsh1236I  
 acII  
 hgaI  
 thai  
 fnuDII/mvni  
 bstUI  
 bsh1236I  
 nruI  
 bsh1236I  
 foki haeIII/pali  
 haeI  
 101 CAAACGTTTC GCGCAGAAGC AGGCCATTAT  
 GCGCGCATG GCGGCCGACG CGCTGGGCTA CGTCTTGCTG GCGTTCGCA CGCGAGGCTG GATGCCCTC  
 GTTTGAAG CCGCTCTTCG TCCGGTAATA GCGCGGTAC GCGCGGCTG CCGACCCGAT GCAGACGAC CGCAAGCGCT GCGCTCCGAC CTACCGGAAG

FIG. 41K

3201 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA GGCCATGCTG TCCAGGCAGG TAGATGACGA CCATCAGGA CAGCTTCAAG  
GGGTAACTACT AGAAGAGCGG AGGCCCGCGG TAGCCCTACG GGCGCAACGT CCGGTACGAC AGGTCGGTCC ATCTACTGCT GGTAGTCCCT GTCGAAGTTC

301 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAAACG GGTGGCATG  
CTACCGAGCG CCGAGAATGG TCGGATTGNA GCTAGTGACC TGCGGACTAG CAGTGCCGCT AAATACGGCG GAGCCGCTCG TGTACCTGC CCAACCGTAC

1 GATTGTAGGC GCGCGCTAT ACCTTGTCTG CCTCCCGCGG TTGGCTCGCG GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAAGCCGG CGGCACCTCG  
CTAACNTCCG CCGCGGATA TGGAACAGAC GGAGGGGCGC AACCGAGCG CACGTACCTC CACGTACCTC GGCCCGTGG AGCTGGACTT ACCTTCGGCC GCCGTGGAGC

FIG. 41L

[illegible]

sau3AI  
 mboI/ndeII(dam-)  
 mamI(dam-)  
 dpuI(dam+)  
 dpnII(dam-)  
 bstYI/xhoII  
 alwI(dam-)  
 mspI  
 hpaII  
 mroI bsaBI(dam-)  
 bspMII  
 bspEI(dam-)  
 bsaWI sfaNI  
 accIII(dam-)  
 fnu4HI  
 bsoFI  
 bbvI  
 sfaNI  
 foki  
 cac8I  
 CTGTGGTCCG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCACCG CCCTGCACCA TTATGTTCG GATCTGCATC GCAGGATGCT GTGGGTACC  
 ACCAGAACCC AAAGGCACAA AGCATTTTCAG ACCTTTGCCG CTTCACTCGC GGGACGTGGT AATACAAGGC CTAGACGTAG CGTCTACGA CGACCGATGG  
 3801

mboII  
 bpuAI  
 bbsI  
 accII  
 thaI  
 fnuDII/mvni hinPI  
 bstUI hhaI/cfoI  
 bsh1236I haeII mslI  
 cac8I  
 hinPI  
 hhaI/cfoI  
 tru9I haeII  
 msel eco47III  
 CTGTGGNACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCCTGAG TGATTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCCTCA  
 GACACCTTGT GCATGTAGAC ATAATTGCTT CGCGACCGTA ACTGGGACTC ACTAAAAGA GACCAGGGCG GCGTAGGTAT GCGGTCAAC AAATGGGAGT  
 3901

maeII  
 bsrI  
 bslI  
 maeII  
 pspl406I maeIII nspHI  
 CAACGTTCCA GTAACCGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG CATCTCTCT CTGTTTCATCG GTATCATTCAC CCCCATGAAC AGAATTCCTC  
 GTTGCAGGT CATTCGCCG TACAAGTAGT AGTCATTGGG CATAGCACTC GTAGAGAGA GCAAGTAGC CATAGTAATG GGGGTACTTG TCTTTAAGG  
 001

nspI  
 scrFI  
 nciI  
 mspI  
 hpaII  
 dsav nlaIII  
 cauII  
 mnlI  
 foki  
 sfaNI  
 maeII  
 mnlI  
 nlaIII  
 apoI  
 bslI

FIG. 41N

[illegible]



[illegible]

FIG. 41P

[illegible]

FIG. 41Q

[illegible]

FIG. 41B

[illegible]

FIG. 41S

001 ATTCTCTTAC TGTCAATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG TACTCMACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC  
 TAAGAGANTG ACAGTACGGT AGGCATTCTA CGAAGAGACA CTGACCACTC ATGAGTTGGT TCAGTAAGAC TCTTATCACA TAGCGCGCTG GCTCAACGAG

mcrI  
 bsiEI  
 bciI  
 fnu4HI  
 bsoFI  
 aciI

rsaI  
 bsrI  
 scaI  
 maeIII  
 hphI  
 csp6I  
 ddeI

fokI  
 nlaIII  
 sfaNI  
 hpaII  
 hpaII  
 scrFI  
 nciI  
 dsaV

hgaI  
 hincII/hindII  
 hincII/acyI  
 hincII/bsaHI  
 mspI  
 hpaII  
 scrFI  
 nciI  
 dsaV

hinPI  
 hhaI/cfoI  
 thaI  
 fnuDII/mvnI  
 bstUI  
 bshI236I  
 aciI

hgaI/aspHI  
 bspI286  
 bsiHKAI  
 tru9I  
 mseI  
 bmyI  
 ahaIII/draI  
 asp700  
 mboII

maeII  
 pspI406I  
 xnnI

sau3AI  
 mboI/ndeII[dam-]  
 dpaI[dam+]  
 dpaII[dam-]  
 bstYI/xhoII  
 alwI[dam-]

01 TTGCCGCGG TCAACACGGG ATATACCGG GCCACATAGC AGAATCTTAA AAGTGCTCAT CATTGGGAAA CGTTCTTCGG GCGGAAAAC CTCAAGGATC  
 AACGGGCGG AGTTGTGCCC TATTATGGCG CGGTGTATCG TCTTGAAATT TTCACGAGTA GTAACCTTTT GCAAGAAGCC CCGCTTTTGA GAGTTCTCTAG

bsrI  
 sau3AI  
 taqI  
 mboI/ndeII[dam-]  
 dpaI[dam+]  
 dpaII[dam-]  
 alwI[dam-]  
 bstYI/xhoII  
 aciI

hgaI/aspHI  
 bspI286  
 bsiHKAI  
 bmyI  
 apaLI/snoI  
 alw44I/snoI  
 dpaII[dam-]  
 dpaII[dam-]  
 bstYI/xhoII  
 maeIII  
 bssSI

hphI  
 hphI

nspBII  
 aciI

TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCCACTG ATCTTCAGCA TCTTTTACTT TCACCCAGCGT TTCTGGGTGA GCAAAAACAG  
 AATGGCGACA ACTCTAGGTC AAGCTACATT GGTGAGCAGC GTGGGTTGAC TAGMAGTCGT AGAAAATGNA AGTGGTCCGA AAGACCCACT CGTTTTTGTG

mboII  
 eaiI/ksp632I  
 sspI

aciI  
 fnu4HI  
 bsoFI

mslI  
 gaaGGCAAAA  
 TGCCGCAAAA  
 CTTCCGTTTT

gaaGGCAAAA  
 TAGGGTAATA  
 CTTCCCTATT  
 CCGGCTGTGC  
 CTTTACNACT  
 TATGAGTATG  
 AGAAGGAAA  
 AGTTATATA  
 ACTTCGTAAA  
 TAGTCCCAAT

TCAATATTAT  
 TGAACCATTT  
 ATCAGGGTTA

FIG. 41T

6401	TTGTCTCATG	AGCGGATACA	TATTTGAATG	TATTTAGTAA	ATAAACAATA	TAGGGTTTCC	GCGCACATTT	CCCCGAAAAG	TGCCACCTGA	CGTCTAAGAA
	AACAGAGTAC	TGCGCTATGT	ATAAACTTAC	ATAAATCTTT	TTATTTGTTT	ATCCCCAAGG	CGCGTGTAAG	GGGGCTTTC	ACGGTGGACT	GCAGATTCTT

6501	ACCATTTATTA	TCATGACATT	AACCTATATA	AATAGGCGTA	TCACGAGGCC	CTTTCGTCTT	CMA
	TGGTAATAAT	AGTACTGTAA	TTGGATATTT	TTATCCGCAT	AGTGCTCCGG	GAAAGCAGAA	GTT

nlaIII rcaI bspHI bsmAI bsrBI	hinPI thal fnuDII/mvnI bstOI bsh1236I aciI nlaIV hhaI/cfoI	maeII hinII/acyI ahaII/bsaHI aatII ddeI
-------------------------------------------	---------------------------------------------------------------------------------	--------------------------------------------------

nlaIII rcaI bspHI mseI	sau96I haeIII/palI asuI ecoO109I/draII mnlI bssSI bbsI	mboII bpuAI bbsI
---------------------------------	--------------------------------------------------------------------------	------------------------

(SEQ ID NO: 61)

FIG. 41U

```

>length: 6563

aatII(GACGTC): 1645 6489
acc65I(GGTACC): 403 823
accI(GTMKAC): 1093 1963 4449
accIII(TCCGGA): 3867[dam-]
acII(CCGC): 178 542 805 877 1340 1750 1826 2011 2039 2043 2182 2242 2384 2492 2501 2504
2628 2781 2784 2787 2906 2926 3005 3045 3094 3141 3226 3241 3309 3342 3367 3412
3436 3448 3490 3544 3597 3613 3619 3700 3838 3967 3970 3981 4139 4155 4210 4266
4351 4390 4400 4442 4467 4505 4518 4544 4561 4604 4611 4632 4723 4751 4878 4897
5018 5128 5263 5272 5634 5725 5916 5962 6083 6127 6204 6313 6412 6459
see hinI
acyI 1307 4678
afIIII(ACRYGT): 1788
ageI(ACCGGT): 1645 1813 2616 2637 2751 3408 6107 6489
ahaII/bsaHI(GRCGYC): 1645 1813 2616 2637 2751 3408 6107 6489
ahaIII/draI(TTTAAA): 5435 5454 6146
ahdI/eam1105I(GACNNNNNGTC): 346 5566
72 121 252 320 398 532 589 648 1126 1144 1167 1325 1386 1906 2054 2075 2126
2218 2233 2889 3292 4202 4259 4270 4319 4338 4619 4845 4935 4981 5238 5759 5859
5922
aluI(AGCT): 1831 4494 4992 6238
412 413 712 713 1171 1471 2578 2579 3300 3870 5245 5319 5331 5416 5429 5893
6196 6214
alw44I/snoI(GTGCAC): 1117 1385 5089
alwI[dam-](GGATC): 1695
1831 4494 4992 6238
1 391 4093
alwNI[dcn-](CAGNNNCTG): 1117 1385 5089
apaI(GGGCCC): 1695
1831 4494 4992 6238
1 391 4093
apaLI/snoI(GTGCAC): 1695
1831 4494 4992 6238
1 391 4093
apoI(RAATTY): 1695
1831 4494 4992 6238
1 391 4093
apyI[dcn+](CCWGG): 1695
1831 4494 4992 6238
1 391 4093
aseI/asnI/vspI(ATTAAAT): 5742
asnI 5742
asp700(GAANNNTTC): 905 930 4234 6166
asp718(GGTACC): 403 823
asphI 403 823
aspi 403 823
asui(GGNCC): 1119 1195 1425 1434 1446 1512 1695 1696 1752 2155 2375 2727 3002 3090 3339 3463

```

FIG. 41V

Stop Template Primer

SL.97.2     5' CAT GGT ATA GGT TAA ACT TAT TTA CAC 3' (SEQ ID NO: 63)

NNS Randomization Primer

SL.97.3     5' CAT GGT ATA GGT NNS ACT TAT TTA CAC 3' (SEQ ID NO: 64)

FIG. 42



Randomization of Position N35 of Variable Light Chain CDR-1  
Amino Acid Frequency

*Phage Display (NNS Codon Library) Sort #3*

Amino Acid	Frequency	% Total	IC50 (nM)
Asparagine (wt)	1	5.6	4.9
Glycine	6	16.6	3.1
Aspartic Acid	3	16.6	3.1
Glutamic Acid	4	22.2	0.1
Alanine	2	5.6	0.2
Lysine	1	5.6	ND
Serine	1	1.9	ND

FIG. 43A

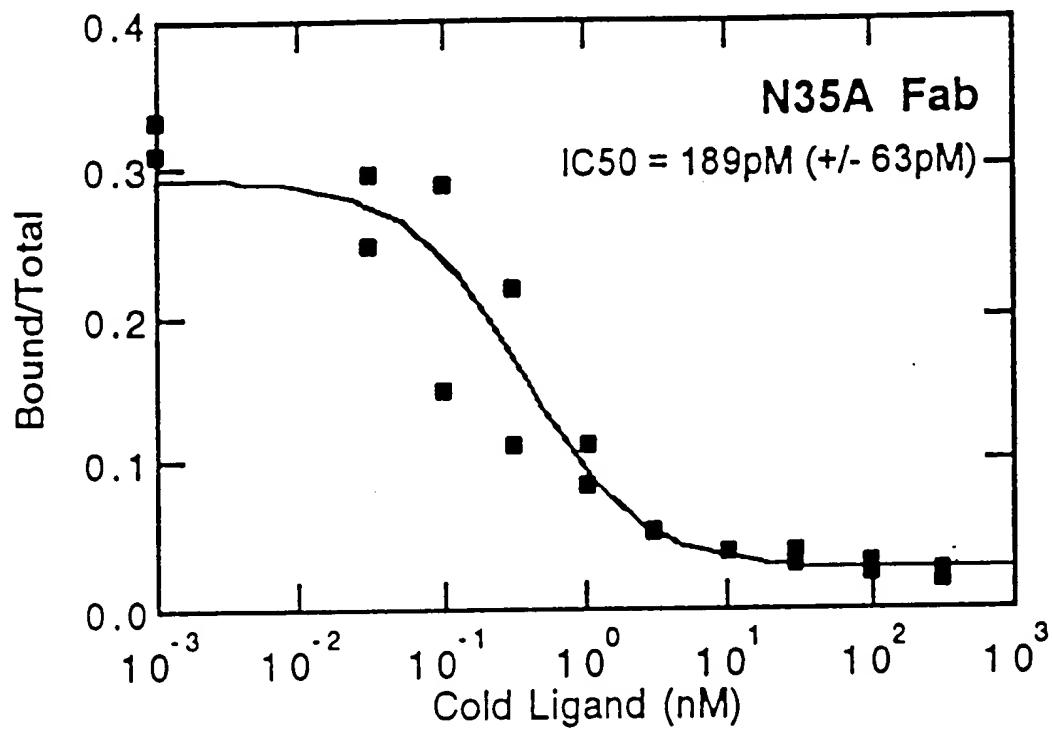


Fig 43B

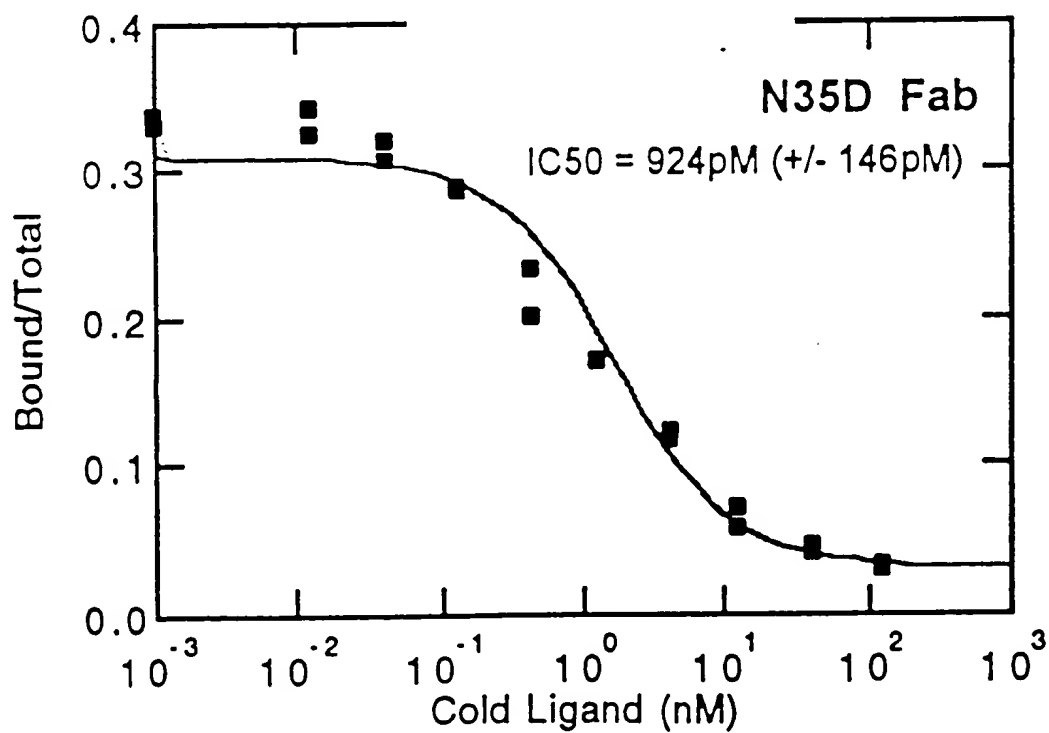


Fig. 43C

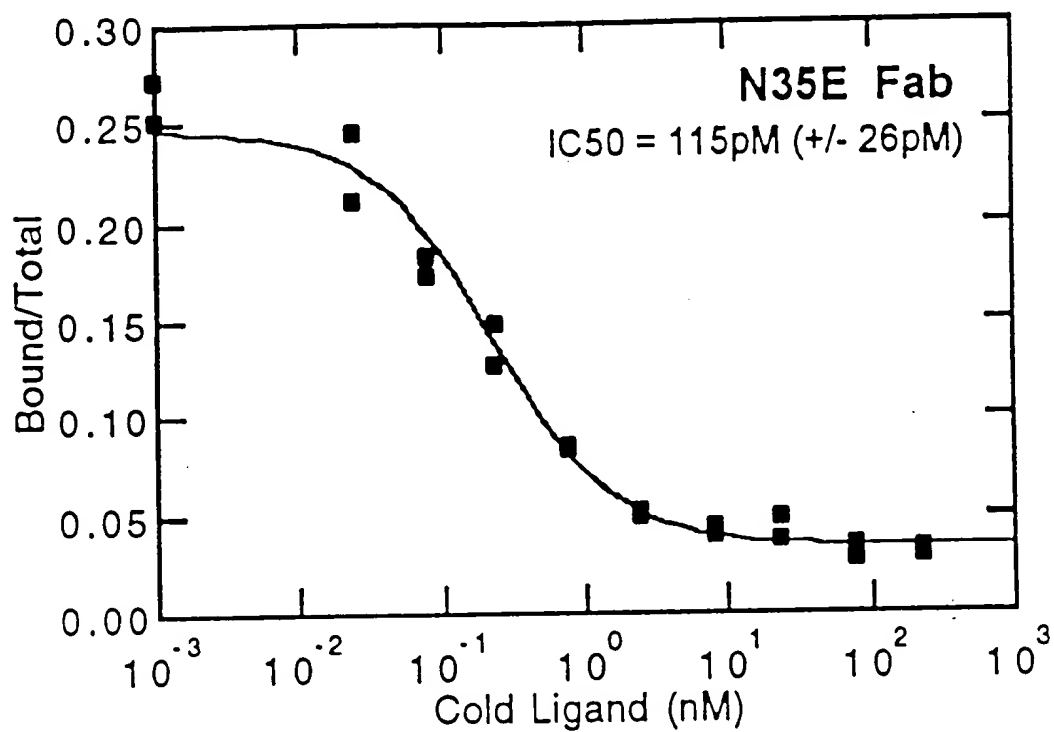


Fig. 43D

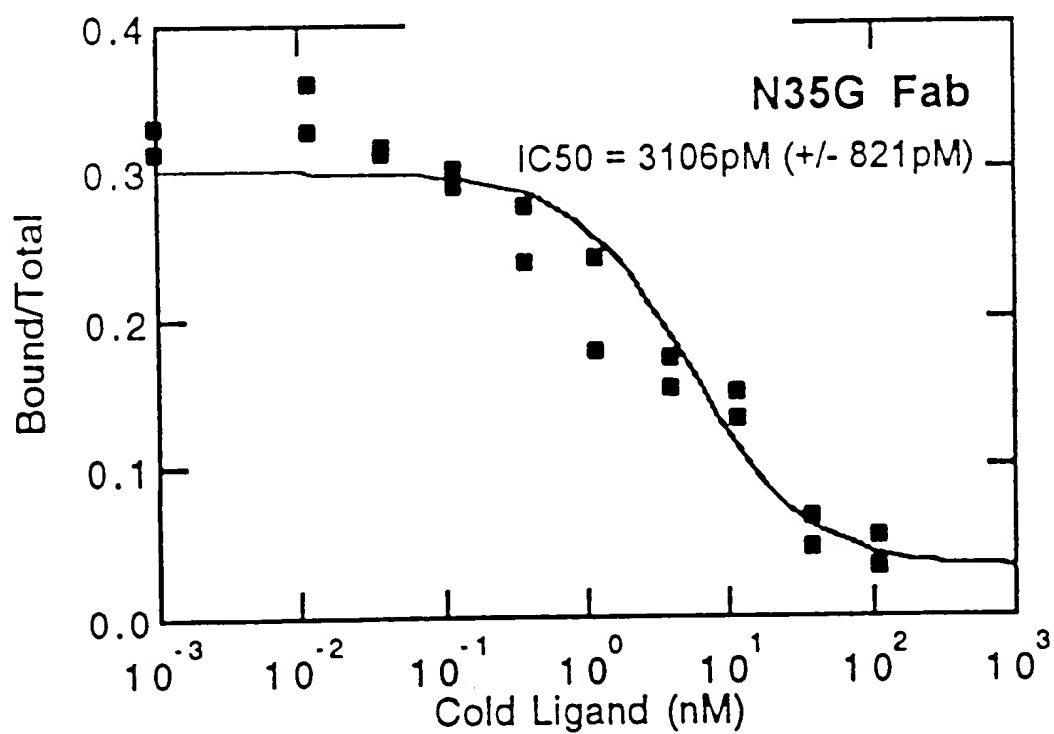
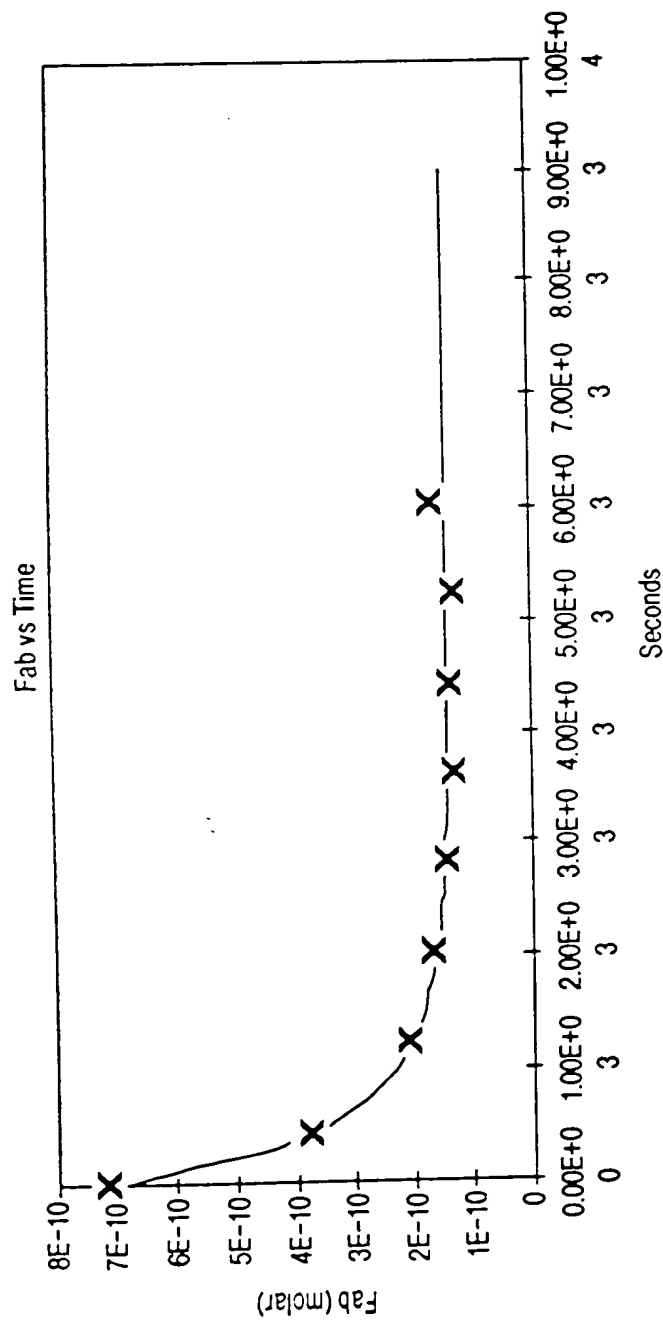


Fig. 43E



Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.F(ab')<sub>2</sub>.

SAMPLE	ka	kd	Kd
6G4V11N35A-Fab	ND	ND	114pM
6G4V11N35A-F(ab') <sub>2</sub>	2.0x10 <sup>6</sup>	2.1x10 <sup>-4</sup>	109pM
6G4V11N35E-Fab	4.7x10 <sup>6</sup>	2.6x10 <sup>-4</sup>	54pM

FIG. 44

1 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC  
 TACTTTTTCT TATAGCGTAA AGAAGAACGT AGATACAAGC AAAAAAGATA ACGATGTTTG  
 -23 M K K N I A F L L A S M F V F S I A T N  
  
 61 GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC TGTCCGCCTC TGTGGGCGAT  
 CGTATGCGAC TATAGGTCTA CTGGGTCAGG GGCTCGAGGG ACAGGCGGAG ACACCCGCTA  
 -3 A Y A D I Q M T Q S P S S L S A S V G D  
  
 121 AGGGTCACCA TCACCTGCAG GTCAAGTCAA AGCTTAGTAC ATGGTATAGG TGAGACGTAT  
 TCCCAGTGGT AGTGGACGTC CAGTTCAGTT TCGAATCATG TACCATATCC ACTCTGCATA  
 18 R V T I T C R S S Q S L V H G I G E T Y  
  
 181 TTACACTGGT ATCAACAGAA ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC  
 AATGTGACCA TAGTTGTCTT TGGTCTTTTT CGAGGCTTTG ATGACTAAAT GTTTCATAGG  
 38 L H W Y Q Q K P G K A P K L L I Y K V S  
  
 241 AATCGATTCT CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT  
 TTAGCTAAGA GACCTCAGGG AAGAGCGAAG AGACCTAGGC CAAGACCCTG CCTAAAGTGA  
 58 N R F S G V P S R F S G S G S G T D F T  
  
 301 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC ACAGAGTACT  
 GACTGGTAGT CGTCAGACGT CGGTCTTCTG AAGCGTTGAA TAATGACAAG TGTCTCATGA  
 78 L T I S S L Q P E D F A T Y Y C S Q S T  
  
 361 CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA TCAAACGAAC TGTGGCTGCA  
 GTACAGGGCG AGTGCAAACC TGTCCCATGG TTCCACCTCT AGTTTGCTTG ACACCGACGT  
 98 H V P L T F G Q G T K V E I K R T V A A  
  
 421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT  
 GGTAGACAGA AGTAGAAGGG CGGTAGACTA CTCGTCAACT TTAGACCTTG ACGAAGACAA  
 118 P S V F I F P P S D E Q L K S G T A S V  
  
 481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC  
 CACACGGACG ACTTATTGAA GATAGGGTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG  
 138 V C L L N N F Y P R E A K V Q W K V D N  
  
 541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC  
 CGGGAGGTTA GCCCATTGAG GGTCCTCTCA CAGTGTCTCG TCCTGTCGTT CCTGTCTGTT  
 158 A L Q S G N S Q E S V T E Q D S K D S T  
  
 601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC  
 ATGTCGGAGT CGTCGTGGGA CTGCGACTCG TTTCGTCTGA TGCTCTTTGT GTTTCAGATG  
 178 Y S L S S T L T L S K A D Y E K H K V Y  
  
 661 GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA  
 CGGACGCTTC AGTGGGTAGT CCCGGACTCG AGCGGGCAGT GTTCTCTGAA GTTGTCCCTT  
 198 A C E V T H Q G L S S P V T K S F N R G  
  
 721 GAGTGTTAAG CTGATCCTCT ACGCCGGACG CATCGTGGCC CTAGTACGCA ACTAGTCGTA  
 CTCACAATTC GACTAGGAGA TCGGGCCTGC GTAGCACCAG GATCATGCGT TGATCAGCAT  
 218 E C O (SEQ ID NO: 62)

(SEQ ID NO: 65)

FIG. 45

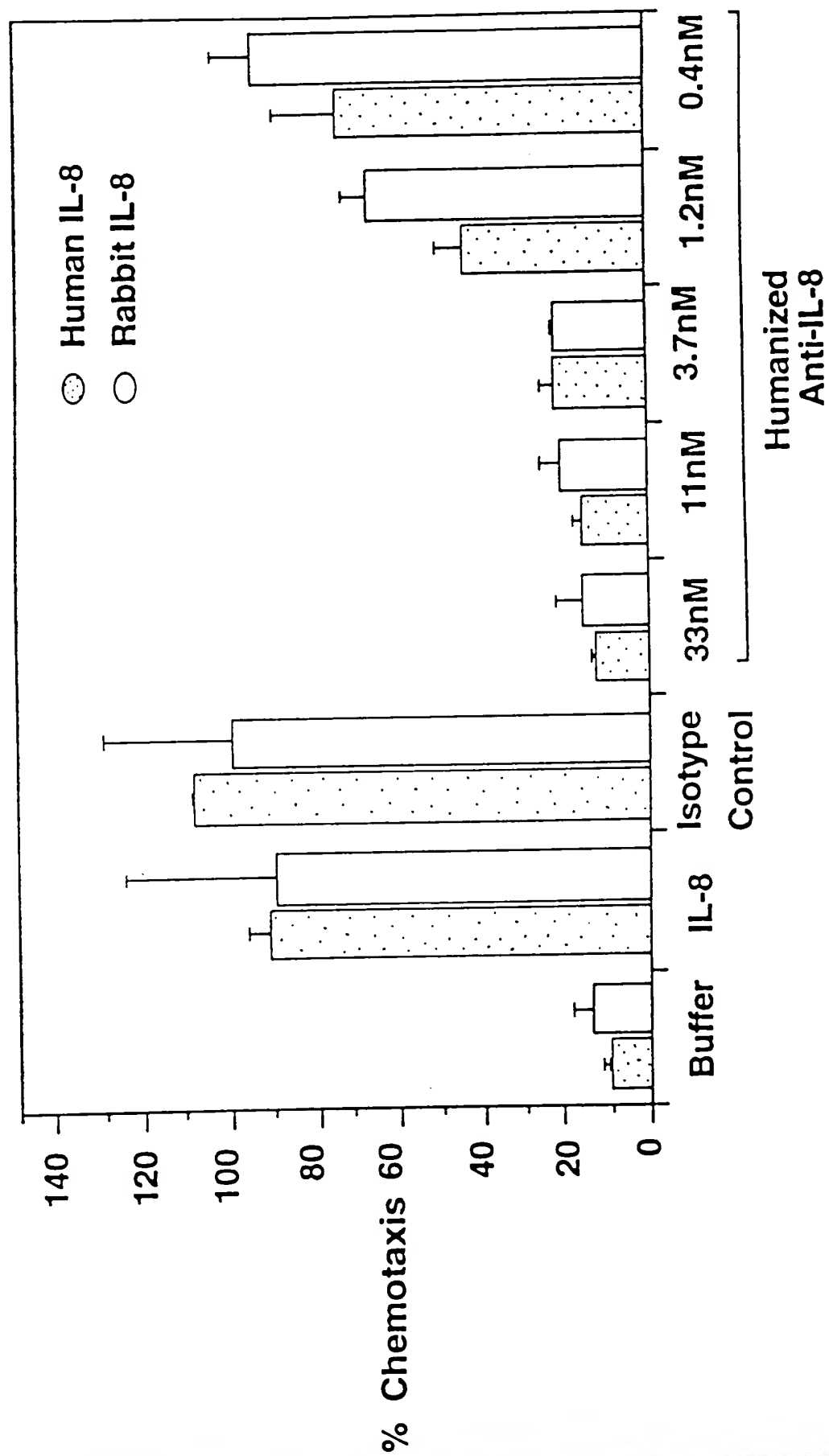


FIG. 46

N35AH1upr

5 CTAGTGCAGTCTGGCGGTGGCCTGGTGCAGCCAGGGGGCTCACTCCGTTTGTCCTGTGCAGCTTCTGGCTACTCCTTC-3' (seq ID NO: 66)

N35AH1lwr

5'-TCGAGAAGGAGTAGCCAGAAAGCTGCACAGGACAACGGAGTGAGCCCCCTGGCTGCACCAGGCCACCGCCAGACTGCACCT  
AG-3'

**Bold indicates nucleotide change destroying PvuII site.**

FIG. 47

> length: 8120 (circular)  
 > This has the pSVI backbone with the PRK7 cloning linker (pSVI7) and the intron DHFR(ID)  
 > made from pSVI.WTSD.D by adding a linearization linker(LL) into the HpaI site

```

cac8I
alul
setI
sacI
hgiJII
hgiAI/aspHI
ecII36II
bspI286
bsiHKAI
bmyI
banII
taqI
1 TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA
AAGCTCGAGC GGGCTGTAAC TAATAACTGA TCTCAGCTAG CTGTGACAC CTTACACACA GTCAATCCCA CACCTTTTCAG GGTCCGAGG GGTCGTCGGT

          sau3AI alul
          mboI/ndeII[dam-]
          dpnI[dam+]
          pvuI/bspCI
          pIeI dpnII[dam-]
          hinfI taqI[dam-]
          rmaI mcrI pvuII
          maeI bsiEI nspBII
          bfaI taqI[dam-]
          scrFI
          mvaI
          ecorII
          dsav
          bstNI
          apyI[dcm+]
          bsaJI
          bsmFI nlaIV
          cac8I
          ppulOI
          nsiI/avaIII
          nlaIII
          sphi
          nspI
          nspHI
          cac8I
          sexAI
          bsmFI nlaIV
          cac8I
          CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTC AGGGGTCGGA GGGGTCGTC CAGCAGCAGG GTGTGGAAAG TCCCAGGCT CCCGAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
          101 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCGAG GTGTGGAAAG TCCCAGGCT CCCGAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA
          CTTCATACGT TTCGTACGTA GAGTTAATCA GTCGTTGGTC CACACCTTC AGGGGTCGGA GGGGTCGTC CAGCAGCAGG GTGTGGAAAG TCCCAGGCT CCCGAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA

          nlalII
          styI
          ncoI
          bslI dsal
          aciI bsaJI
          201 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCCAAGTC CGCCCATCTCT CCGCCCATCT CCGCCCATCT GCTGACTAAT TTTTTTTTAT
          CAGTCGTTGG TATCAGGGCG GGGATTGAGG CCGGTAGGCG GGGATTGAG GCGGTCGAG GCGGGTGA GA GCGGGGTAC GCGCTGATTA AAAAAAATAA

```

FIG. 48A



301 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG  
 ATACGTCTCC GGCTCCGGCG GAGCCGGAGA CTCGATNAGG TCTTCATCAC TCCTCCGAAA AAACCTCCGG ATCCGAAAAC GTTTTCGAT CGAATAGGCC  
 501 CCGGGACCGG TGCATTGGAA CGCGGATTCC CGCTGCCAAG AGTGACGTAA GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT  
 GGCCCTTGCC ACCTAACCTT CGCGCTAAGG GGCACGGTTC TCACTGCATT CATGGCGGAT ATCTCGCTAT TCTCTAANA TAGGGCGAC GGTACTACCA  
 DHFR ATG<sup>+</sup>

Restriction sites (enzyme names) are indicated above the sequence. The sequence is presented in two lines, with the first line containing the first 301 bases and the second line containing the next 200 bases (501-701). The sequence is flanked by the DHFR ATG start codon.

FIG. 48B

601 CAAAGAATGA CCACACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT TATGGGTAGG AATACCTGGT TCTCCATTCC TGAGAAAGAT CGACCTTTAA  
GTTTCTTACT GGTGTTGGAG AAGTCACCTT CCATTGTCT TAGACCACCTA ATACCCCATCC TTTTGGACCA AGAGGTAAGG ACTCTTCTTA GCTGGAAATT

701 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCMAAGA ACCACCACGA GGAGCTCATTT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA  
TCCTGCTTA ATTATATCAA GAGTCATCTC TTGAGTTTCT TGCTGGTGCT CCTCGAGTAA AAGACGGTT TTCMAACCTA CTACGGAATT CTGAATAACT

801 ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA GTTCTGTTTA CCAGGAGGCC ATGANTCAAC CAGGCCACCT TAGACTCTTT  
TGTTGGCTT AACCGTTTAT TTATCTGTGA CCAACCTAT CAGCTCCGT CAAGACAAAT GGCTCTCGG TACTTAGTTG GTCCGGTGA ATCTGAGAA

```

          hgaI
          hlnII/acyI
          ahaII/bsaHI
scrFI
mvaI      mnlI
ecorII
dsaV
bstNI     ecoNI
          apyI[dcm+] mnlI
          bsaJI     bslI ddeI
          mnlI
          901 GTGACAAGGA TCATGACGGA ATTTGAAAGT GACACGTTTT TCCACAGAAAT TGATTTGGGG AAATATAAAC CTCTCCACAG ATACCCAGGC GTCTCTCTGTG
          CACTGTTCCT AGTACGTCCT TAACTTTTCA CTGTGCNAAA AGGCTCTTTA ACTAANCCCC TTTATATTG GAGAGGGTCT TATGGGTCCG CAGGAGAGAC

          nlaIII
          sau3AI
          mboI/ndeII[dam-]
          dpnI[dam+]
          dpnII[dam-]
          maeIII alwI[dam-] apoI      maeIII
          maeIII
          901 GTGACAAGGA TCATGACGGA ATTTGAAAGT GACACGTTTT TCCACAGAAAT TGATTTGGGG AAATATAAAC CTCTCCACAG ATACCCAGGC GTCTCTCTGTG
          CACTGTTCCT AGTACGTCCT TAACTTTTCA CTGTGCNAAA AGGCTCTTTA ACTAANCCCC TTTATATTG GAGAGGGTCT TATGGGTCCG CAGGAGAGAC

          scrFI
          mvaI
          ecorII
          dsaV
          bstNI
          apyI[dcm+]
          sau96I
          auaII
          asuI      mnlI      sfaNI      mboII      aluI
          1001 AGGTCCAGGA GGAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGNAG AAAGACTAAC AGGAGATGC TTTCAAGTTC TCTGCTCCC TCCTAAAGCT
          TCCAGGTGCT CCTTTTCCG TAGTTCATAT TCNAACTTCA GATGCTCTTC TTCTGTGATTG TCCTTCTACG AAAGTTCAG AGACGAGGGG AGGATTTCGA
          ^END DHR

          atyI
          bsaJI
          sau3AI
          mboI/ndeII[dam-]
          dpnI[dam+]
          dpnII[dam-]
          alwI[dam-]
          bstYI/xhoII
          cac8I
          dsal bsmFI
          bsaJI
          nlaIII
          styI
          ncoI
          ppulOI
          nslI/avaIII
          1101 ATGCATTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCTTGG CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATACAC
          TACGTAAAAA TATTCTGGTA CCCTGAAAAC GACCGAAATC TAGGGGACC GAAGCAATCT TCGGTGATG TTAATTATGT ATTGGAATAC ATAGTATGTG

          sau96I
          auaII
          asuI
          scrFI
          mvaI
          ecorII

```

FIG. 48D

1201 ATACGATTTA GGTGACACTA TAGATAACAT CCACCTTTGCC TTCTCTCCCA CAGGTGTCCA CTCACAGGTC CAACCTGCAC TCGGTTCTAT CGATTGAAAT  
TATGCTAAAT CCACCTCTGAT ATCTATTGTA GGTGAAACGG AAAGAGAGGT GTCCACAGGT GAGGCTCCAG GTTGACGTGG AGCCAAAGTA GCTAACTTAA  
seq from PRK6G425VH: Cla-AvrII^

nlaIII  
 etyI  
 pflMI  
 ncoI  
 dsal  
 bsaJI foki  
 nlaIII foki  
 CCACCATGGG ATGGTCATGT ATCATCCTTT  
 GGTTGGTACCC TACCAGTACA TAGTAGGAAA AAGATCATCG TTGACGTTGA CCTCATGTAA GTCTTCAAGT CGATCAGGTC AGACGCCAC CGGACACGT  
 1301

[illegible]

FIG. 48E

bslI  
 sau3AI  
 mboI/ndeII[dam-]  
 dpnI[dam+]  
 dpnII[dam-]  
 alwI[dam-] hphI  
 1501 TGGGTTGGAT ATATTGATCC TTCCATGGT GAACTACGT ATATCAAAA GTTCAGGGC CGTTTCACTT TATCTCGGA CAACCTCCAA AACACAGCAT  
 ACCCAACCTA TATACTAGG AAGGTACCA CTTTGATGCA TATTAGTTT CAAGTTCCCG GCNAAGTGAA ATAGAGCGCT GTTGAGGTTT TTGTGTCGTA  
 47 W V G Y I D P S N G E T T Y N Q K F K G R F T L S R D N S K N T A Y  
 hnlII/acyI  
 ahalI/baHI  
 aatII  
 bsrI  
 maeIII  
 taqI  
 hphI  
 mboII maeII  
 bspMI  
 cac8I ddeI drdI  
 1601 ACCTGCAGAT GAACAGCCTG CGTGCTGAGG ACACCTGCCG CTATTACTGT GCNAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG  
 TGGAGCTCTA CTTGTCGAC GCACGACTCC TGTGACGCA GATAATGACA CGTTCTCCCC TAATAGCGAT GTTACCACCT ACCAAGAGC TGCAGACCCC  
 81 L Q M N S L R A E D T A V Y Y C A R G D Y R Y N G D W F F D V W G  
 scrFI  
 mvaI  
 ecorII  
 dsav  
 bstNI  
 bsaJI  
 sau96I  
 haeIII/palI  
 asuI  
 fnu4HI  
 bsoFI  
 bsp1286 aciI bsaJI  
 bmyI nspBII apyI[dcm+]  
 1701 TCNAGGACC CTGGTCACCG TCTCTCGGC CTCCACCMAG GCGCCATCGG TCTTCCCCCT GGCACCTCC TCCACAGACA CCTCTGGGG CACAGCGGCC  
 AGTTCTTGG GACCACTGGC AGAGGAGCCG GAGGTGGTTC CCGGGTAGCC AGAAGGGGA CCGTGGAGG AGGTTCTCGT GGAGACCCCG GTGTCGCCG  
 114 Q G T L V T V S S A S T K G P S V F P L A P S S K S T S G G T A A

FIG. 48F

[illegible]

FIG. 48G

[illegible]

[illegible]



```

2701 TCCCTGTCTC CGGGTAATG AGTGGGACGG CCCTAGATC GACCTGCAGA AGCTTGCCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
AGGGACAGAG GCCCATTTAC TCACCGTGGC GGGATCTCAG CTGGACGTCT TCGAACCGGC GGTACCGGGT TGAACCAATA ACGTCCAATA TTACCAATGT
447 S L S P G K O (SEQ ID NO: 71)

sau96I          acII  haeIII/palI
fnu4HI          asuI
bsoFI nlalII
sfilI styI
eaeI ncoI
cfrI dsal
aluI haeIII/palI
hindIII bglI bsaJI
asuI bfaI accI bspMI
bmiAI          bali cauII
bali cauII
2701 TCCCTGTCTC CGGGTAATG AGTGGGACGG CCCTAGATC GACCTGCAGA AGCTTGCCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA
AGGGACAGAG GCCCATTTAC TCACCGTGGC GGGATCTCAG CTGGACGTCT TCGAACCGGC GGTACCGGGT TGAACCAATA ACGTCCAATA TTACCAATGT
447 S L S P G K O (SEQ ID NO: 71)

sfaNI apoI          rmaI
maeI
bsmI bfaI          nlalII alwI{dam-}

2801 AATAAGCAA TAGCATCACA AATTTCACMA ATAAAGCATT TTTTCACTG CATTCTAGTT GTGGTTTGT CAAACTCATC AATGTATCTT ATCATGTCTG
TTATTTCTGTT ATCGTAGTGT TTAAAGTGTT TATTTCTGTA AANAAGTGAC GTAAAGATCA CACCAACACAG GTTTGAGTAG TTACATAGAA TAGTACAGAC

sau3AI          mboI/ndeII{dam-}
dpmI{dam+}
dpmII{dam-}
pvuI/bspCI
mcrI
baeI
taqI{dam-} tru9I
claiI/bsp106{dam-}
bspDI{dam-} maeI
sau3AI xmiI
mboI/ndeII{dam-}
dpmI{dam+} asp730
dpmII{dam-} aaeI/asnI/vspI bsaJI
2901 CATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT GAAAGAGGMA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG
CTAGCTAGCC CTTAATTAG CCGCGTCTGT GTACCGGACT TTATGGAGA CTTTCTCCTT GAACCAATCC ATGGAAGACT CCGCCTTTCT TGGTAGACAC

rsal
csp6I
nlalV
kpnI
hglCI
bani
asp718 mnlI
acc65I ddeI acII

```

FIG. 48J

3001 GAATGTGTGT CAGTTAGGCT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA GAACTATGCA AAGCTGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG bsmFI  
CCTACACACA GTCAATCCCA CACCTTTCAG GGGTCCGAGG GGTGCTCCGT CTTCATACGT TTCTGACGTA GAGTTATCA GTCGTTGGTC CACACCTTTC

3101 TCCCGAGGCT CCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA GTCAGCAACC ATACTCCCG CCCTAACTCC GCCATCCG CCCCTAACTC acII  
AGGGTCCGA GGGTCCGCTC GTCTTCATAC GTTTCGTAGC TAGAGTTAAT CAGTCGTTGG TATCAGGCG GGGATTGAGG CGGGTAGGCG GGGGATTGAG

3201 CGCCAGTTC CGCCCATTTCT CGGCCCATG CCGCCCATG GCTGACTAAT TTTTCTTAT TATGCAGAGG CCGAGGCCG CTGCGCTCT GAGCTATTCC AGAAGTAGTG bseRI  
GCGGGTCAAG GCGGGTAAGA GCGGGGTAC CGACTGATTA AAAAAATAA ATACGTCTCC GGTCTCCGCG GAGCCGGAGA CTCGATAAGG TCTTCATCAC

```

3301 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAGAAGCTA GCTTATCCGG CCGGAGACGG TCGATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA
TCCGCCGAA ANACCTCCGG ATCCGAAAC GTTTTTCGAT CGATAGGCC GGCCTTGCC ACGTACCTT GCGCCTAAGG GGCAGGTTT TCAGTCCATT
^seq from pSV16B5-6G4VL: AvrII - HindIII frag
^U1 matched splice donor^

3401 GTACCGCCTA TAGAGTCTAT AGGCCACCC CCTTGGCTTC GTTAGACGC GGCTACAATT ATACATAAC CTTTGGATC GATCCTACTG ACACTGACAT foki
CATGGCGGAT ATCTCAGATA TCCGGGTGGG GGAACCGAAG CAATCTTGG CCGATGTTAA TTATCTATTG GAAACCTAG CTAGGATGAC TGTGACTGTA
^removed ATG ^U2 match
^ap6 promoter
^ariat consensus^
IqG vH natural lariet restored^

```

FIG. 48L



mepI  
hpaII  
bslI  
bsaWI  
sau3AI  
mboI/ndeII[dam-]  
dpnI[dam+]  
dpnII[dam-]  
alwI[dam-]  
nlaIV  
bstYI/xhoII  
bamHI  
alwI[dam-] bsmFI  
TCTCTCGCT TCTCTGGATC CGTTCTGCG AC GGATTTC A CTCTCAACCAT CAGCAGTCTG  
GGAA GAGCGA AGAGACCTAG GCCAAGACC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC

tfII  
hinfi  
taqI  
clai/bep106 pIei  
bspDI[dam-] hinfi  
CCATCGATT CTCTGGAGTC CCTTCTCGCT

3801 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT TCTCTGGATC CGTTCTGCG AC GGATTTC A CTCTCAACCAT CAGCAGTCTG  
TGATCACTAA ATGTTTCATA GGTTAGCTAA GAGACCTCAG GGAA GAGCGA AGAGACCTAG GCCAAGACC TGCCTAAAGT GAGACTGGTA GTCGTCAGAC

51 L L I Y K V S N R F S G V P S R F S G S G S G T D F T L T I S S L

rbaI  
csp6I  
nlaIV  
kpnI styI  
hgICl  
banI bsaJI  
asp718  
acc65I  
maeII  
GGACAGGTGA CCAGGTGGA  
CCTGTGCCAT GTTCCACCT

rsal  
csp6I  
nlaIV  
kpnI styI  
hgICl  
banI bsaJI  
asp718  
acc65I  
maeII  
GGACAGGTGA CCAGGTGGA  
CCTGTGCCAT GTTCCACCT

3901 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA cscAI nlaIII maeII  
GTGGTCTTC TGAAGCGTTG AATAATGACA AGTCTCTCAT GAGTACAGGG CGAGTGCANA CTTGTGCCAT GTTCCACCT

84 Q P E D F A T Y Y C S Q S T H V P L T F G Q G T K V E I K R T V A A

mboII  
bpuAI  
bbal  
mboII  
bpuAI  
bbal  
xmnI  
asp700  
cacBI  
xmnI  
asp700

4001 CACCATCTGT CITCATCTTC CCGCCATCTG ATGAGCACTT GAATCTGGA ACTGCTTCTG TTGTGSCCT GCTGAATAAC  
GTGGTAGACA GAAGTAGAAG GCGGGTAGAC TACTCTCAA CTTTAGACCT TCACGMAGAC AACACACGA CGACTTATTG

118 P S V F I F P P S D E Q L K S G T A S V V C L L N N F Y P R E A K

haeIII/palI  
haeI  
mnlI  
TTCTATCCCC GAGAGGCCAA  
AAGATAGGCT CTCTCCGGTT

scrFI  
 mvaI  
 ecorII  
 dnaV  
 bstNI  
 apyI[dcn+]

4101 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA GTGTCACAGA GCAGGACAGC AAGGACAGCA CCGTCTGTCT CCGTCTGTCT GGTATGTCGA GTGTCGTGG

151 V Q W K V D N A L Q S G N S Q E S V T E Q D S K D S T Y S L S S T

rsaI  
 csp6I  
 mnlI  
 bali  
 maeIII bsaJI  
 maeIII

4201 CTGACGCTGA GCAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCCTGCGA AGTCACCCAT TCAGTGGGTA GTCCCGGACT CGAGCGGCA GTGTTCTCG AAGTTGTCCC

184 L T L S K A D Y E K H K V Y A C E V T H Q G L S S P V T K S F N R G

ddeI  
 celII/espl  
 bplI/bpull102I  
 hgaI  
 sstI  
 sacI  
 hgiJII  
 hgiAI/aspHI  
 eclI36II  
 bspI286  
 bsiHKA I  
 bmyI  
 ddeI cac8I  
 haeIII/pali  
 sau96I aluI  
 asuI banII  
 ecoO109I/draII  
 alwNI[dcn-]  
 maeIII  
 aluI

4301 GAGAGTGTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTTACA AATTAAGCAA TAGCATCACA AATTTCACA ATAAAGCATT

218 E C O (Seq ID no: 72)

aluI  
 fnu4HI  
 bsoFI  
 bbvI  
 maeIII  
 sfaNI apoI

FIG. 480

**FIG 48D**

4701 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC CGCCAGTTTC CGCCCATTTCT CGCGCCCATG GCTGACTAAT  
TAGAGTTAAT CAGTCGTTGG TATCAGGGCG GGGATTGAG CGGGTAGGGC GGGGATTGAG CGGGGTCAAG GCGGGGTAC GCAGTGATTA

4801 TTTTTTTTATT TATGCAGAGG CCGAGGGCGC CTCGGCTCT GAGCTATTCC AGAGTAGTGT AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGAGCTG  
AAAAAATAA ATACGTCTCC GGCTCCGGCG GAGCGGAGA CTCGATAAGG TCTTCATCAC TCCTCCGAA AACCTCCG ATCCGAAAC GTTTTCGAC  
start pUC118~

4901 TTACCTCCAG CGCGCGCTTA ATTAAGCGC GCCATTAA TCCTGCAGGT AACAGCTTGG CACTGGCCGT CGTTTACAA CTCGTGACT GGAAGACCC  
AATGGAGCTC GCGGGGAAT TAATTCCGG CGGTAAATT AGCAGTCCA TTGTGAACC GTGACCGCA GCAATATGT GCAGCACTGA CCCTTTTGGG  
^linearization linker inserted into HpaI site





mspI  
hpaII  
naeI  
cfrI01/bsrFI  
maeII cac8I  
5301 TTTCTCGCCA CGTTCGCCG CTTTCCCGT CAAAGCTTAA ATCGGGGGCT CCCTTTAGG TTCCGATTGA GTGCTTTACG GCACCTCGAC CCCAAAAAAC  
AAAGAGCGGT GCAAGCGGCC GAAAGGGCA GTTCGAGATT TAGCCCCCGA GGGAAATCCC AAGGCTAAAT CACGAAATGC CGTGGAGCTG GGGTTTTTTG  
nlaIV  
hgiCI taqI  
bani mnlI  
nlaIV  
hgiCI taqI  
bani mnlI  
maeII haeIII/palI  
draIII sau96I  
5401 TTGATTTGGG TGATGGTTCA CGTAGTGGC CATCGCCCTG ATAGACGGTT TTTGGCCCTT TGACGCTTGA GTCCACGTTT TTTAATAGTG GACTCTTGT  
AACTAAMCCC ACTACCAAGT GCATCACCG GTAGCGGGAC TATCTGCCAA AAGCGGGA ACTGCACCT CAGGTGCAAG AAATTATCAC CTGAGAACNA  
hphI  
bsaAI  
maeII pleI  
drdI hinfI maeII msel  
tru9I msel  
pleI  
hinfI  
bsrI  
bslI  
5501 CCAAACTGGA ACACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT AAGGATTTT GCCGATTTCG GCCTATTGGT TAAAAAATGA GCTGATTAA  
GGTTTGACCT TGTGTGAGT TGGGATAGAG CCGGATAAGA AACTAATAA TTCCCTAATA CCGCTAAGC CGGATAACCA ATTTTACT CGACTAAAT  
truuI  
msel  
haeIII/palI  
hgiAI/aspHI  
bsp1286  
bslIHKAI  
bmyI ddeI  
apaLI/snoI rsaI  
alw44I/snoI csp6I  
5601 CAAAAATTTA ACGCGAATTT TAACAAATA TTAACGTTTA CAATTTTATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAATCC  
GTTTTAAAT TGCCTTAA ATTGTTTTAT AATTGCAAT GTTAAATATC CACGTGAGAG TCATGTTAGA CGAGACTAGC GCGTATCAAT TCGTTGAGG  
thai  
fnuDII/mvni  
tru9I apoI tru9I  
msel bstUI msel  
apoI bsh1236I sspI msel  
6000 CAAAAATTTA ACGCGAATTT TAACAAATA TTAACGTTTA CAATTTTATG GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAATCC  
GTTTTAAAT TGCCTTAA ATTGTTTTAT AATTGCAAT GTTAAATATC CACGTGAGAG TCATGTTAGA CGAGACTAGC GCGTATCAAT TCGTTGAGG  
fnu4HI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCTATCGCTA CGTGACTGG TCATGGCTGC GCGCGGACAC CCAGCAACAC CCCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGCATC CGCTTACAGA  
CGATAGCAT GCACTGACCC AGTACCGAG CGGGGCTGTG GCGGCTGTG GCGGACTGCG CGGACTGCC CGAACAGACG AGGCGGTAG CGCAATGTCT  
hinPI  
fnu4HI  
bsaAI  
bsaAI tthIII/aspI bbvI  
5701 GCT

FIG. 48S

**FIG 48T**

sau3AI nspBII mboI/ndeII{dam-} dpnI{dam+} bstYI/xhoII bsrI dpnII{dam-} maeIII taqI alwI{dam-} acII bstYI/xhoII  
 mboI/ndeII{dam-} dpnI{dam+} dpnII{dam-} alwI{dam-} bstYI/xhoII  
 bssSI maeIII taqI alwI{dam-} acII bstYI/xhoII  
 5201 CACGAGTGGG TTACATCGGA CTGGATGCA ACAGCGGTAA GATCCTTGAG AGTTTCGCC CCGAAGNACG TTTTCNATG ATGAGCACTT TTAAGTTCT  
 GTGCTCACCC ATGTAGCTT GACCTAGAGT TGTGGCCATT TGTGGCCATT CTAGGAACCT TCAAAAGCGG GGCTTCTTGC AAAAGTTAC TACTCGTGAA AATTCAAGA  
 sau3AI maeII psp14061 xmnI asp700 mboII  
 hglAI/aspHI bsp1286 tru9I bslHKAI maeI bmyI ahaIII/draI  
 acII nclI mspI hpaII dsav  
 hlnII/acyI hlnPI bsh1236I hhaI/cfoI  
 hgaI caulI ahaII/bsaHI  
 mcrI fnu4HI bcoI bseI bsoFI  
 acII fnu4HI bsoFI  
 mcrI fnu4HI bsoFI  
 bseI  
 rsaI csp6I bsrI  
 scaI hphI maeIII  
 6301 GCTATGTGC GCGGTATTAT CCCGTGATGA CGCCGGGCA GAGCAACTCG GTCGCCGCAT ACACCTATTCT CAGAAATGACT TGTTGAGTA CTCACCCAGTC  
 CGATACACC CGCCATAATA GGGCACTACT CGGCCCGCT CTCGTTGAGC CAGCGCGGTA TGTGATAGA GTCTTACTGA ACCNACTCAT GAGTGGTCAG  
 sau3AI mboI/ndeII{dam-} dpnI{dam+} dpnII{dam-} pvuI/bspCI mcrI bseI  
 haeIII/palI eaeI cfrI fnu4HI bsoFI acII  
 6401 ACAGAAAGC ATCTTACGA TGGCATGACA GTAAGAGAAAT TATGCAGTGC TGCCATAACC ATGAGTGATA ACACCTGCCG CAACCTACTT CTGACACGA  
 TGTCTTTTCG TAGAATGCCT ACCGTACTGT CATCTCTCTTA ATACGTACCG ACGGTATGG TACTCACTAT TGTGACGCCG GTTGAATGAA GACTCTTGCT  
 sfaNI foki nlaIII  
 sau96I avaiI asuI mnlI aluI acII  
 sau3AI maeIII mboI/ndeII{dam-} dpnI{dam+} dpnII{dam-} alwI{dam-} nlaIII  
 6501 TCGGAGGACC GAAGGAGCTA ACCGCTTTT TGCAACACAT GGGGATCAT GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGATGAAG CCATACCAAA  
 AGCCTCCTGG CTTCCTCGAT TGGCAAAA ACGTGTTGTA CCCCCTAGTA CATTGACCG CATTGACMA CTTGGCCTC GACTTACTTC GGTATGTTT

[illegible]

FIG. 48V

sau3AI  
mboII[dam-]  
sau3AI mboI/ndeII[dam-] thaI fnuDII/mvni  
mboI/ndeII[dam-] bstUI cac8I  
dpnI[dam+] dpnI[dam+] fnu4HI  
dpnII[dam-] dpnII[dam-] bshI236I fnu4HI  
bstYI/xhoII alwI[dam-] hlnPI bsoFI  
alwI[dam-] bstYI/xhoII hhaI/cfoI bbvI  
7101 TCAAGGATC TTCTTGAGAT CCTTTTTC TGCGCGTAAT CTGCTGCTTG CAAACMAAA AACACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA  
AGTTTCCTAG AAGNACTCTA GGAATAAAG ACGCGCATTA GACGACGAAC GTTTGTTTTT TTGTTGCGCA TGCTC3CCAC CAAACAAACG GCCTAGTTCT  
  
7201 GCTACCNACT CTTTTTCCGA AGGTNACTGG CTTACAGCAGA GCGCAGATAC CMAATACTGT CCTTCTAGTG TAGCGCTAGT TAGCGACCA CTTCAAGAAC  
CGATGGTTGA GAAAAGGCT TCCATTGACC GNAGTCTGCT CCGCTCTATG GTTTATGACA GCAAGATCAC ATCCGGTGGT GAAGTTCTTG  
  
7301 TCCTAGCAC CGCTACATA CTCGCTCTG CTAATCCTGT TACCAGTGGC TGCTGCCAGT GCGGATAAGT CGTGTCTTAC CGGTTGGAC TCAGACCAT  
AGACATCGTG GCGGATGAT GGACGAGAC GATTAGGACA ATGGTCAACC ACGACGGTCA CCGCTATTCA GCACAGATG GCCCAACCTG AGTTCTGCTA  
  
7401 AGTTACCGGA TAAGGCGCAG CGCTCGGGCT GAAACGGGGT TTCGTGCACA CAGCCACAGT TGGAGCGAAC GACCTACACC GAACTAGAT ACCTACAGCG  
TCNATGGCT ATTCCGCGTC GCCAGCCCCA CTTGCCCCC AAGACCGTGT GTCGGGTGCA ACCTCGCTTG CTGGATGCG CTTGACTCTA TGGATGCTCG

scrFI  
mvaI  
ecorII  
dsv  
bsaV  
bsaJI  
bsaSI  
hinPI mnlI  
hhaI/cfoI  
aluI apyI(dcm+)

7501 TGAGCATTTGA GAAAGCGCCA CGCTTCCCGA AGGAGAGAAAG GCGGACAGGT ATCCGGTAAAG CGGCACGGTC GGAACAGGAG AGCGCAGCAG GGAGCTTCCA  
ACTCGTNACT CTTTCGGCGT GCGNAGGGCT TCCCTCTTTC 'CGCCTGTCCA TAGGCCATTC GCCGTCCAG CCTTGCTCTC TCGCGTGCTC CCTCGAAGGT

mspI  
hpaII  
bsaI  
bsaWI  
fnu4HI  
bsaFI  
acII

7601 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTGT GATGCTCGTC AGGGGCGCG AGCCTATGGA  
CCCCCTTTGC GGACCATAGA AATATCAGGA CAGCCCAAG CCGTGGAGAC TGAACCTCGCA GCTAAAACCA CTACGAGCAG TCCCCCGCC TCGGATACT

mnII drdI  
hgaI  
sfaNI  
acII  
nlaIV

scrFI  
mvaI  
ecorII  
dsv  
bsaNI  
apyI(dcm+)

7701 AAAAGCCAG CAACCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT TTTGCTCACA TGTCTTTCC TCGGTTATCC CCTGATTCTG TGGATAACCG  
TTTTGCGGTC GTTGGCGCG AAAAATGCCA AGGACCGGA AACGACCGTA AACGAGTGT ACAAGAAAG AGCAATAGG GGAATAAGAC ACCTATTGGC

haeIII/paII  
fnu4HI  
bsaFI  
acII  
thaI bslI  
fnuDII/mvnl  
bsuI  
bsl1236I  
cac8I  
nlaIV  
haeI  
cac8I  
afIII  
nspl  
nspl  
tfII  
hinFI

7801 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCGCGCAGC CGAACGACCG AGCGCAGCGA GTCAGTGAGC GAGGAGCGG AAGAGCGCC AATACGCMAA  
ATAATGGCGG AACTACTC GACTATGGCG AGCGCGTGC GCTTGCTGGC TCGCGTGGCT CAGTCACTCG CTCCTTCGCC TTCTCGCGG TTATGCGTTT

api  
mboII  
earI/ksp632I  
hhaI  
acII  
mnlI  
fnu4HI  
bsaFI  
bbvI  
pleI  
hinPI  
hhaI/cfoI  
mcrI  
bsaI  
bsaI  
acII  
haeII

**FIG. 48X**

```

    thal
    fnuDII/mvnI
    bstUI
    bsh1236I
    hinPI
    hhal/cfoI
    thal
    fnuDII/mvnI          cac8I
    bstUI haeIII/pall    aluI
    bsh1236I          tru9I pvuII
    bslI  eaeI  tfII aseI/asnI/vspI
    acII  cfrI  hinFI mscI  napDI
    7901 CCGCCTCTCC CCGCGGCTTG GCCGATTTCAT TAATCCAGCT GGCACGACAG GTTCCCGAC TGGNAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT
    GCGCGAGAGG GCGCGGCNAC CCGCTAAGTA ATTAGGTCA ATTAGGTCA CCGTGCTGTC CNAAGGGCTG ACCTTTCCGC CGTCACTCGC GTTGGGTTAA TTACACTCAA

    scrFI
    mvaI
    ecorII
    dsav
    nlaIV bstNI
    hgiCI apyI(dcm+)
    banI bsaJI
    8001 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA
    TGGAGTGAGT AATCCGTGGG GTCCGAATG TGMATACGA AGGCCGAGCA TACAACACAC CTTAACACTC GCCTATTGTT AAAGTGTGTC CTTGTGCGAT
    aluI

```

FIG. 48Y



```

tru9I
mseI
aseI/asnI/vspI
xmnl
nlaIII asp700
8101 TGACCATGAT TACGAATTAA (SEQ ID NO:68)
ACTGGTACTA ATGCTTAATT

>length: 8120

aatII(GACGTC): 1690 5947
acc65I(GGTACC): 2969 3967 4529
accI(GTAKAC): 823 1039 2738 4237
acII(CCGC): 217 229 238 250 260 271 317 422 454 485 574 1385 1795 1871 2248 2250 2758 2982
3167 3179 3188 3200 3210 3221 3267 3372 3404 3449 3686 3949 4021 4318 4542 4727
4739 4748 4760 4770 4781 4827 4910 4914 5070 5127 5153 5166 5203 5217 5220 5248
5275 5680 5699 5741 5751 5790 5979 6026 6125 6234 6311 6355 6476 6522 6713 6804
7166 7175 7310 7420 7541 7560 7687 7715 7806 7827 7834 7877 7901 7911 7967 8070
see hlnI
acyI
afII/bfI(CTTAAG): 786
afIII(ACRYGT): 932 7758
ageI(ACCGGT): 1833
ahaII/baHI(GRCGYC): 988 1690 1858 5117 5947 6329
ahaII/draI(TTTAAA): 696 4935 6290 6982 7001
ahdI/eam1105I(GACNNNNNGTC): 2087 6865
aluI(AGCT): 5 44 332 386 390 753 1097 1165 1370 1431 1951 2603 2751 2784 3282 3336 3340
3562 3566 3676 3733 3792 4270 4288 4311 4344 4554 4842 4896 4954 5047 5333 5590
5803 5822 6516 6579 6679 7200 7457 7593 7819 7937 8096
alw44I/anoI(GTGCAC): 1876 5651 6198 7444

```

FIG. 48Z

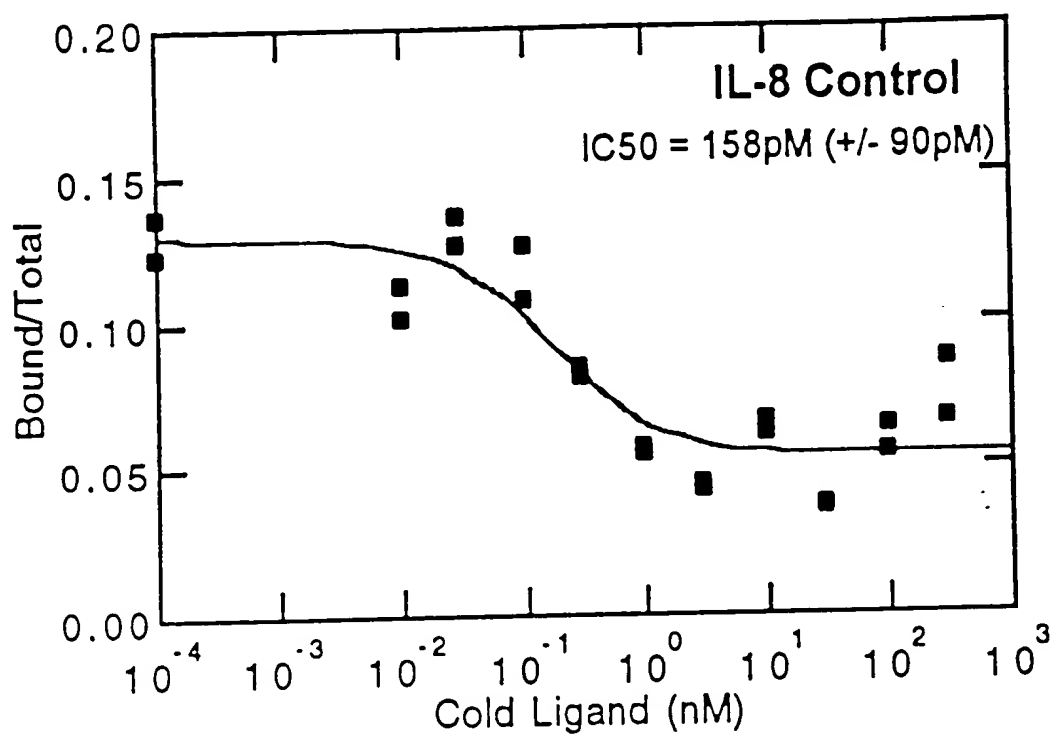


FIG. 49A

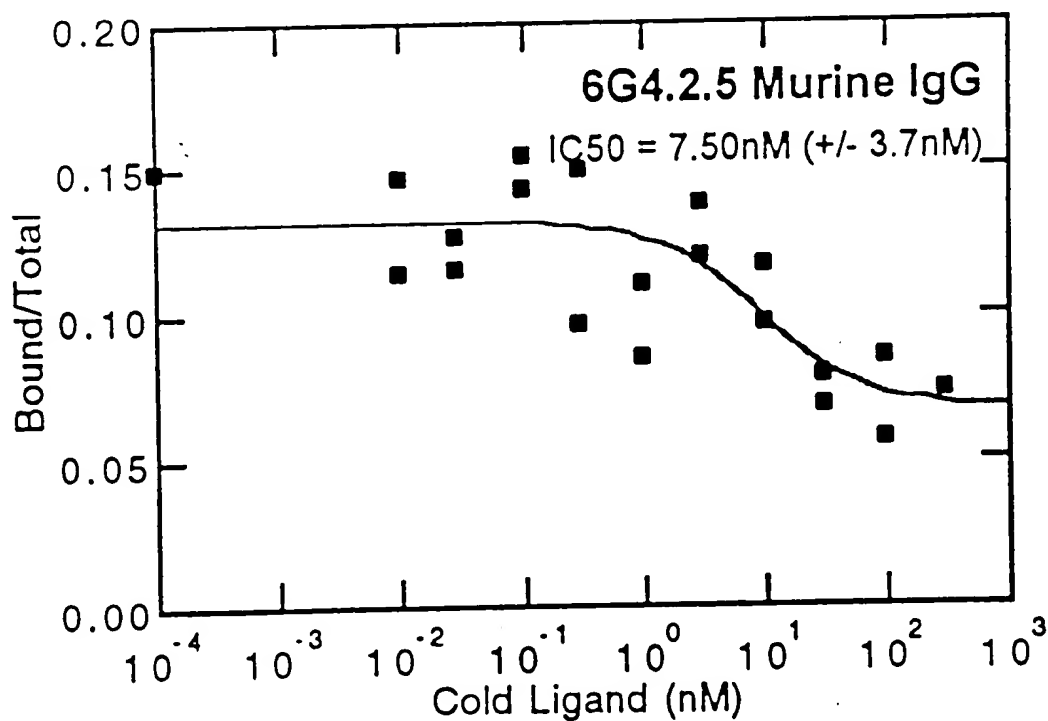


FIG. 49B

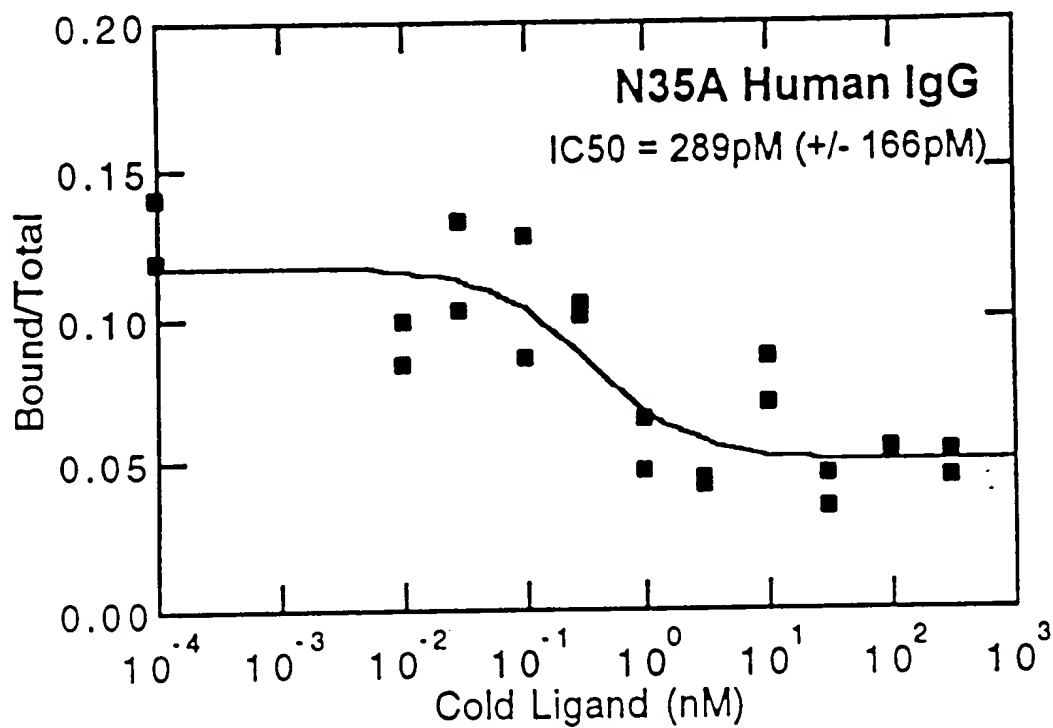


FIG. 49C

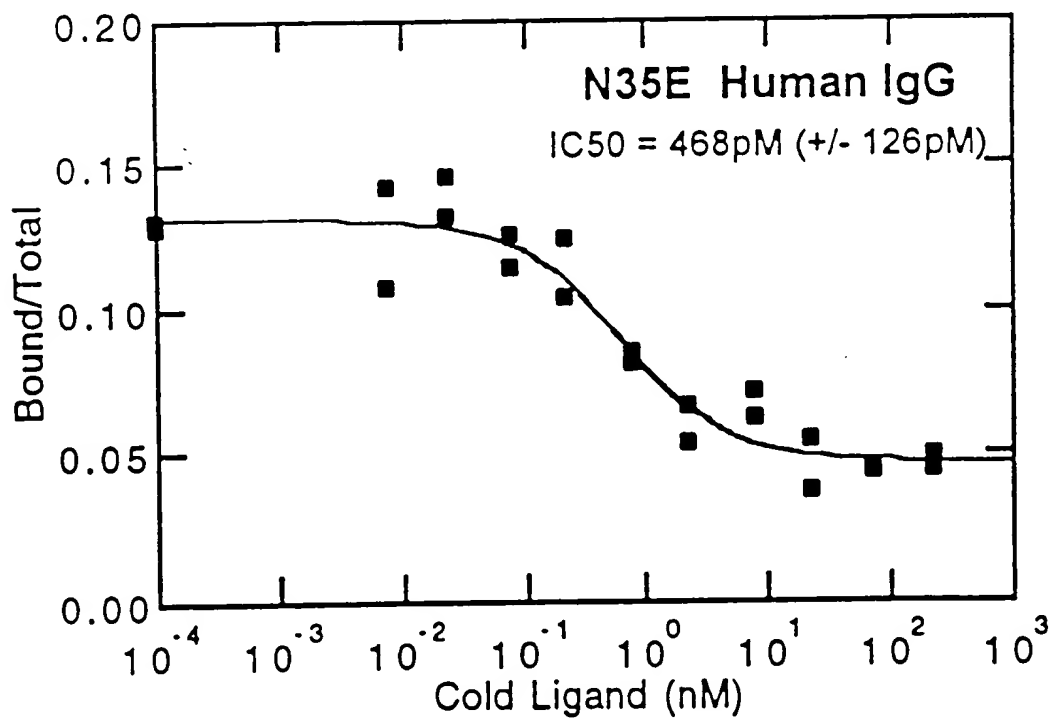


FIG. 49D

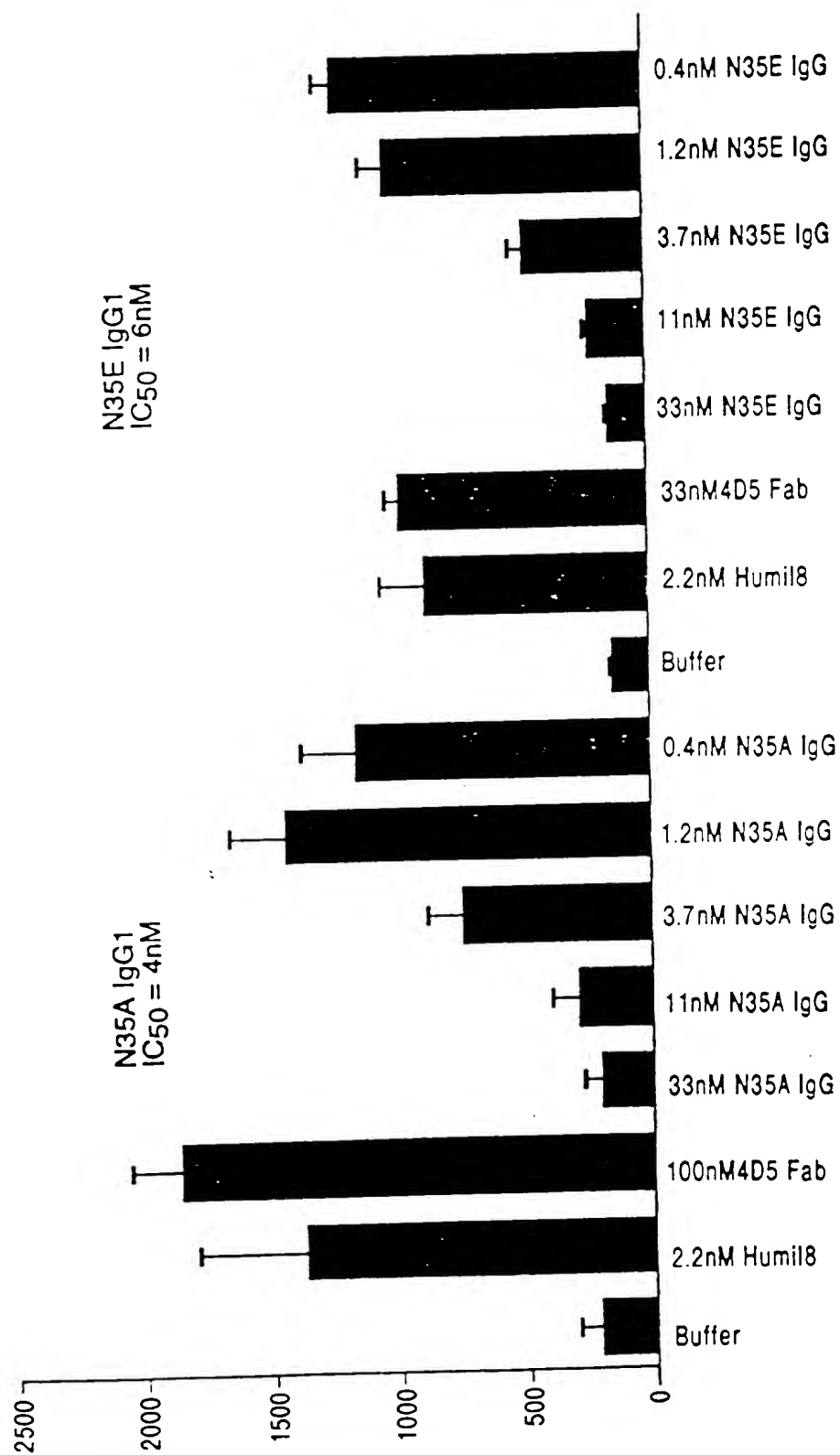


FIG. 50A

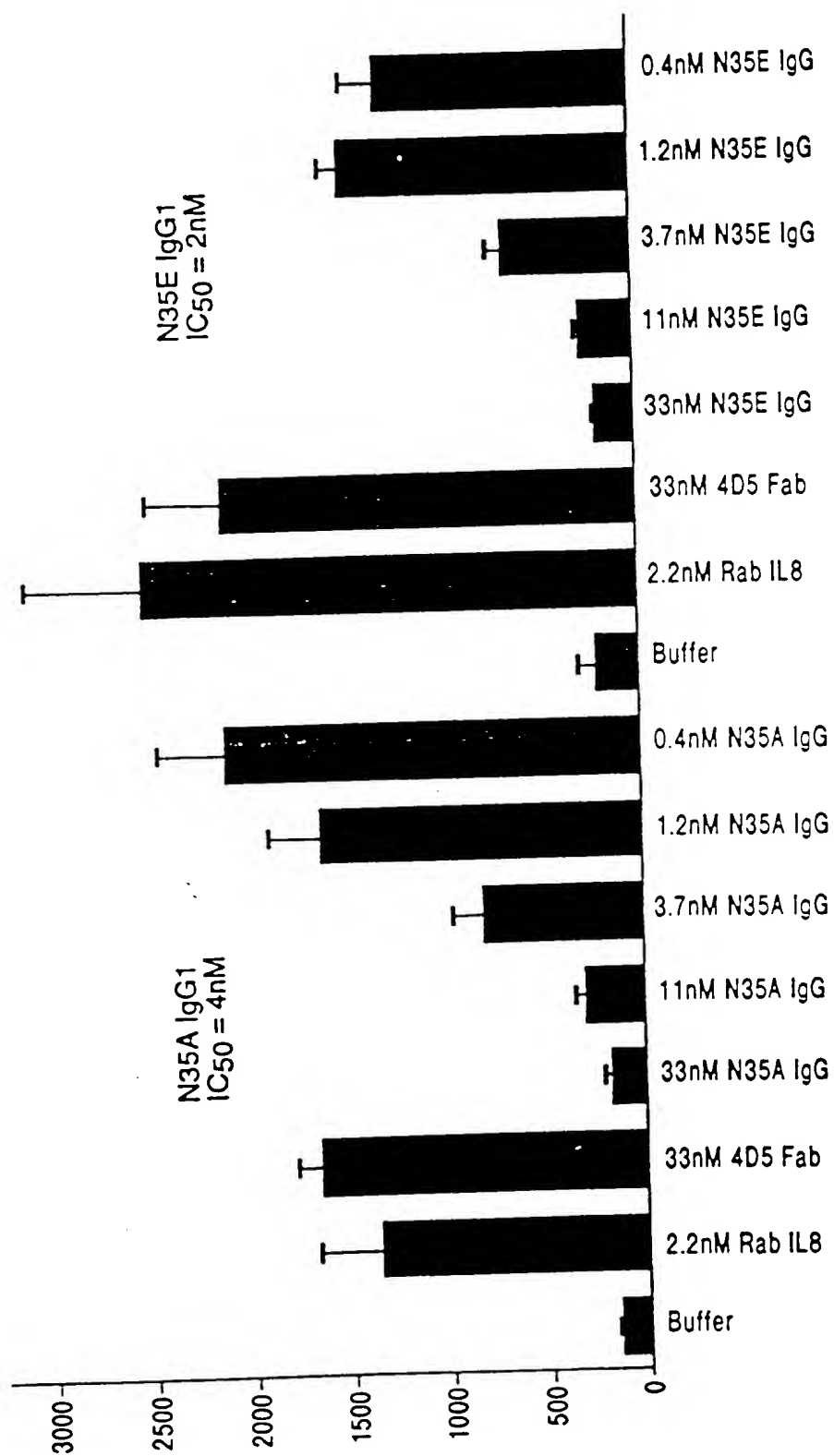
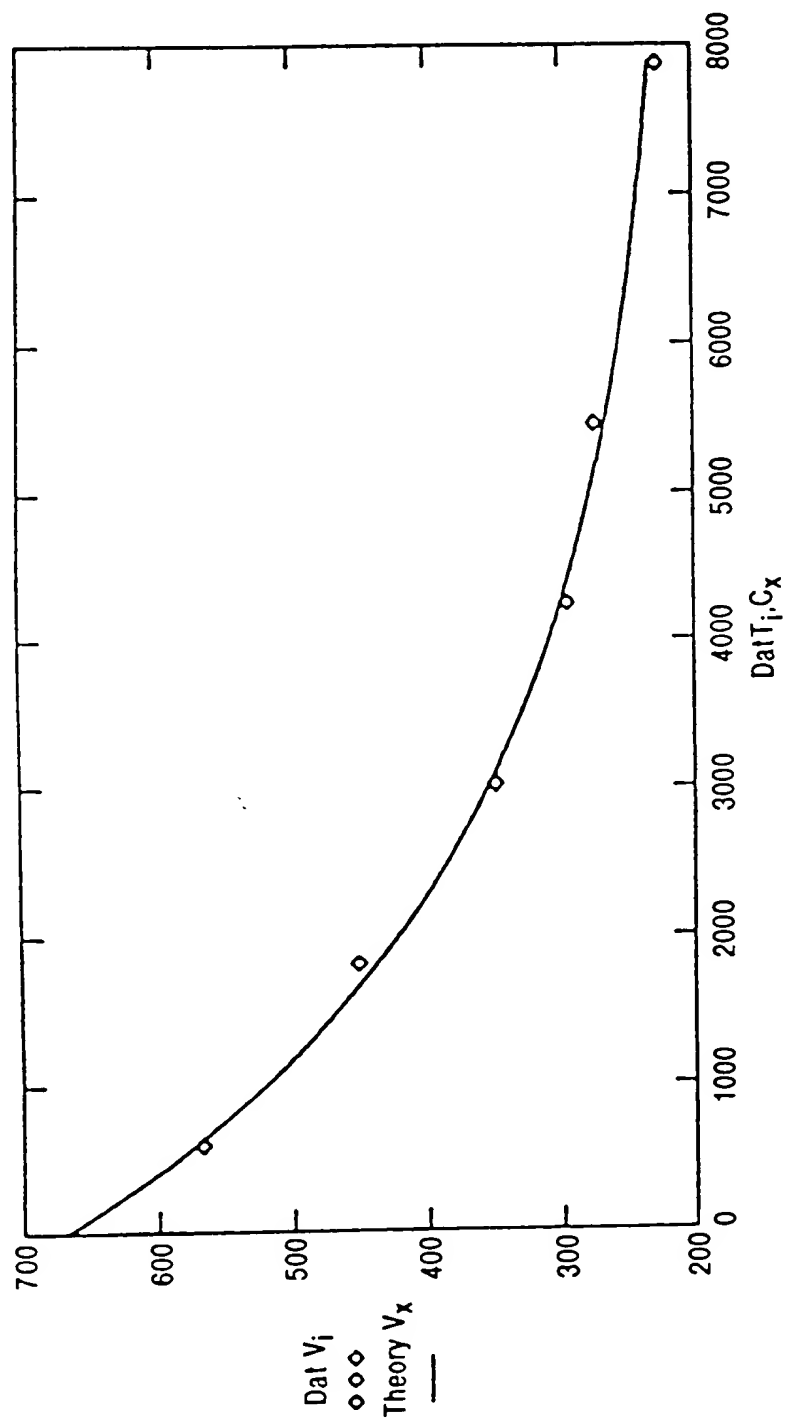


FIG. 50B



**Representative Conc versus Time Plot. Shown is the kinetic data for 6G4V11N35A.IgG1**

SAMPLE	$k_a$	$k_d$	$K_d$
Murine 6G4.2.5 IgG2a	$8.3 \times 10^5$	$2.9 \times 10^{-4}$	350pM
6G4V11N35A-IgG1	$8.7 \times 10^5$	$7.7 \times 10^{-5}$	88pM
6G4V11N35E-IgG1	$3.0 \times 10^6$	$1.4 \times 10^{-4}$	49pM

**FIG. 51**

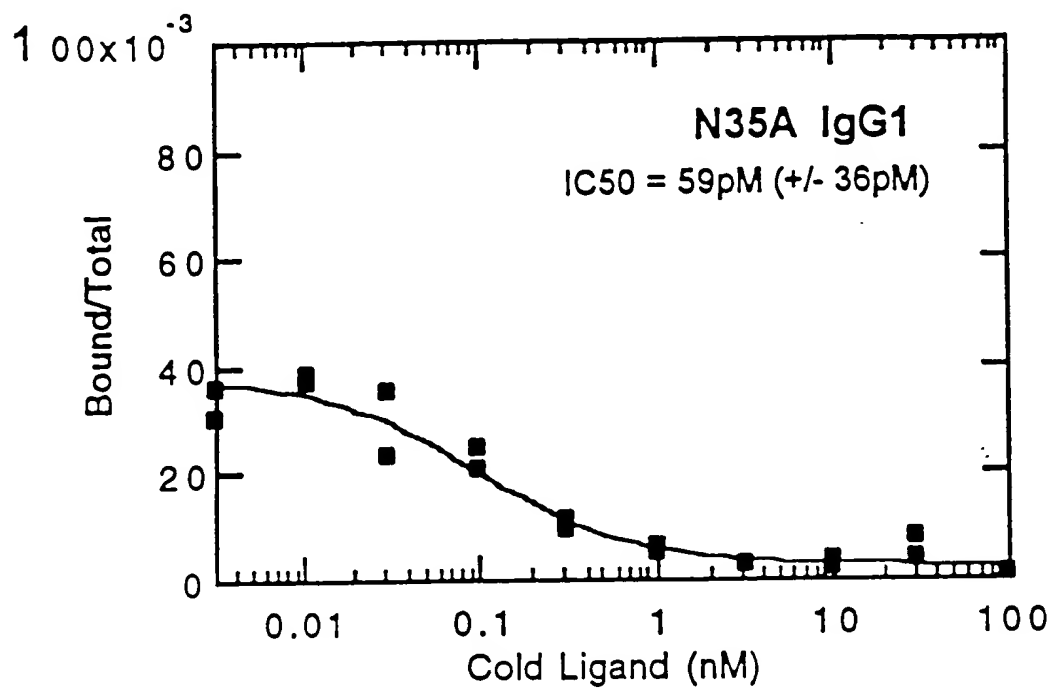


FIG. 52A

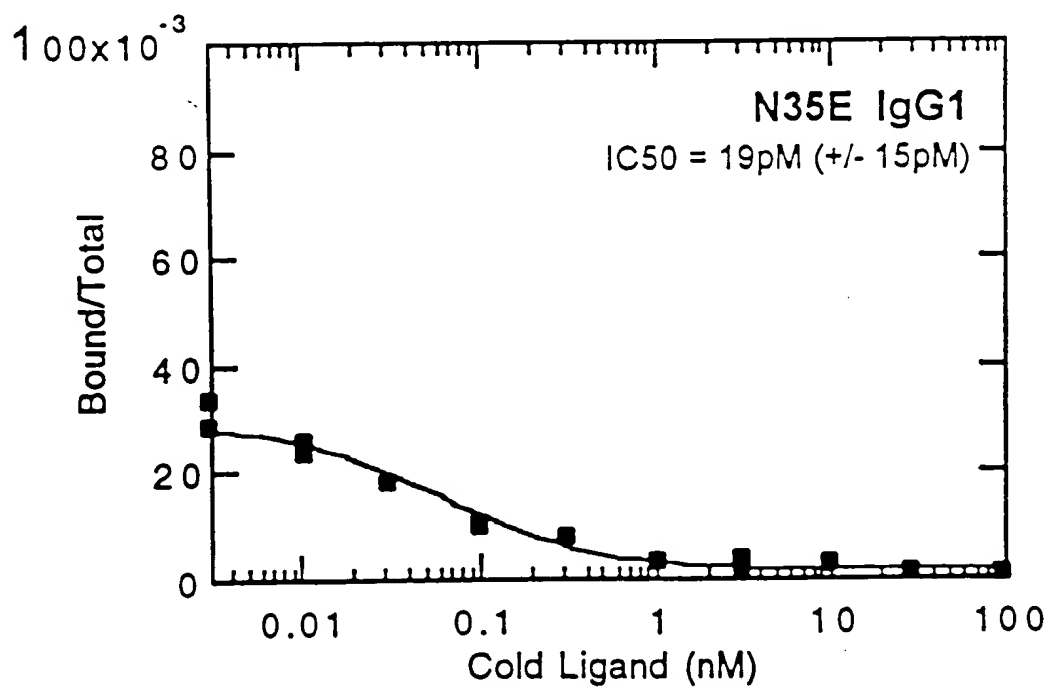


FIG. 52B

781 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT TCTTCCTTGCA  
TTTTCCCATA GATCTCCAAC TCCACTAAAA TACTTTTCT TATAGCGTAA AGAAGAACGT  
-1 M K K N I A F L L A

841 TCTATGTTCTG TTTTTTCTAT TGCTACAAAC GCGTACGCTG AGGTTTCAGCT AGTGCAGTCT  
AGATACAAGC AAAAAAGATA ACGATGTTTG CGCATGCGAC TCCAAGTCGA TCACGTCAGA  
-11 S M F V F S I A T N A Y A E V Q L V Q S

901 GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC  
CCGCCACCGG ACCACGTCGG TCCCCCGAGT GAGGCAAACA GGACACGTCG AAGACCGATG  
8 G G G L V Q P G G S L R L S C A A S G Y

961 TCCTTCTCGA GTCACTATAT GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG  
AGGAAGAGCT CAGTGATATA CGTGACCCAG GCAGTCCGGG GCCCATTCCTC GGACCTTACC  
28 S F S S H Y M H W V R Q A P G K G L E W

1021 GTTGGATATA TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT  
CAACCTATAT AACTAGGAAG GTTACCACTT TGATGCATAT TAGTTTTCAA GTTCCCGGCA  
48 V G Y I D P S N G E T T Y N Q K F K G R

1081 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA CAGCCTGCGT  
AAGTGAAATA GAGCGCTGTT GAGGTTTTTG TGTCGTATGG ACGTCTACTT GTCGGACGCA  
68 F T L S R D N S K N T A Y L Q M N S L R

1141 GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT ATCGCTACAA TGGTGACTGG  
CGACTCCTGT GACGGCAGAT AATGACACGT TCTCCCTAA TAGCGATGTT ACCACTGACC  
88 A E D T A V Y Y C A R G D Y R Y N G D W

1201 TTCTTCGACG TCTGGGGTCA AGGAACCCTG GTCACCGTCT CCTCGGCCTC CACCAAGGGC  
AAGAAGCTGC AGACCCCAGT TCCTTGGGAC CAGTGGCAGA GGAGCCGGAG GTGGTTCCCG  
108 F F D V W G Q G T L V T V S S A S T K G

1261 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG  
GGTAGCCAGA AGGGGGACCG TGGGAGGAGG TTCTCGTGGA GACCCCCGTG TCGCCGGGAC  
128 P S V F P L A P S S K S T S G G T A A L

1321 GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC  
CCGACGGACC AGTTCCTGAT GAAGGGGCTT GGCCACTGCC ACAGCACCTT GAGTCCGCGG  
148 G C L V K D Y F P E P V T V S W N S G A

1381 CTGACCAGCG GCGTGCACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT CTA CTCCCTC  
GACTGGTCGC CGCACGTGTG GAAGGGCCGA CAGGATGTCA GGAGTCTGA GATGAGGGAG  
168 L T S G V H T F P A V L Q S S G L Y S L

1441 AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG  
TCGTGCGACC ACTGGCACGG GAGGTGCTCG AACCCGTGGG TCTGGATGTA GACGTTGCAC  
188 S S V V T V P S S S L G T Q T Y I C N V

1501 AATCACAAGC CCAGCAACAC CAAGGTCGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA  
TTAGTGTTTCG GGTGCTGTG GTTCCAGCTG TTCTTTCAAC TCGGGTTTAG AACACTGTTT  
208 N H K P S N T K V D K K V E P K S C D K

1561 ACTCACACAT GCCCGCCGTGA (SEQ ID NO: 69)  
TGAGTGTGTA CGGGCGGCACT  
228 T H T C P P O  
(SEQ ID NO: 70)

FIG. 53



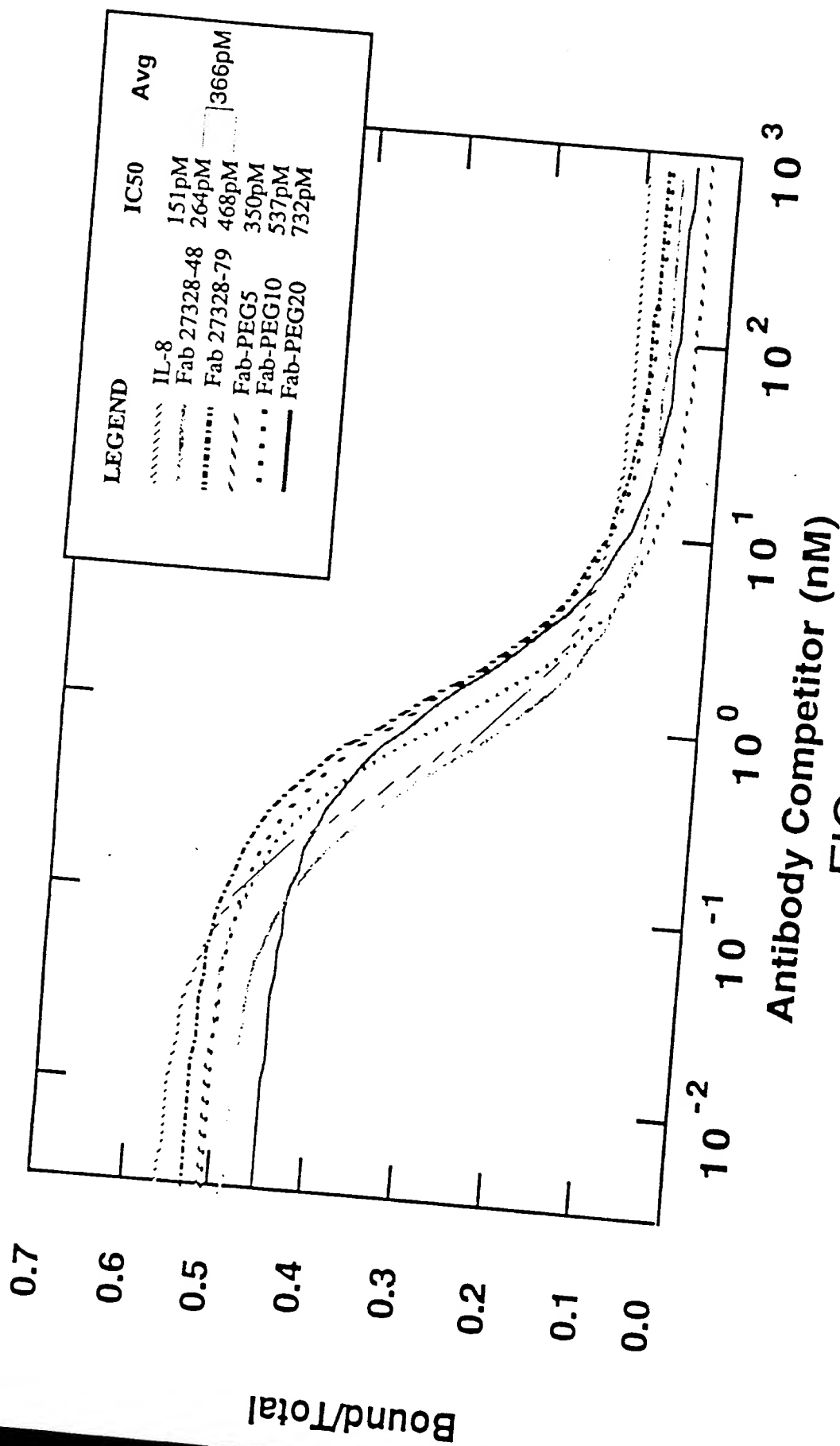


FIG. 54A

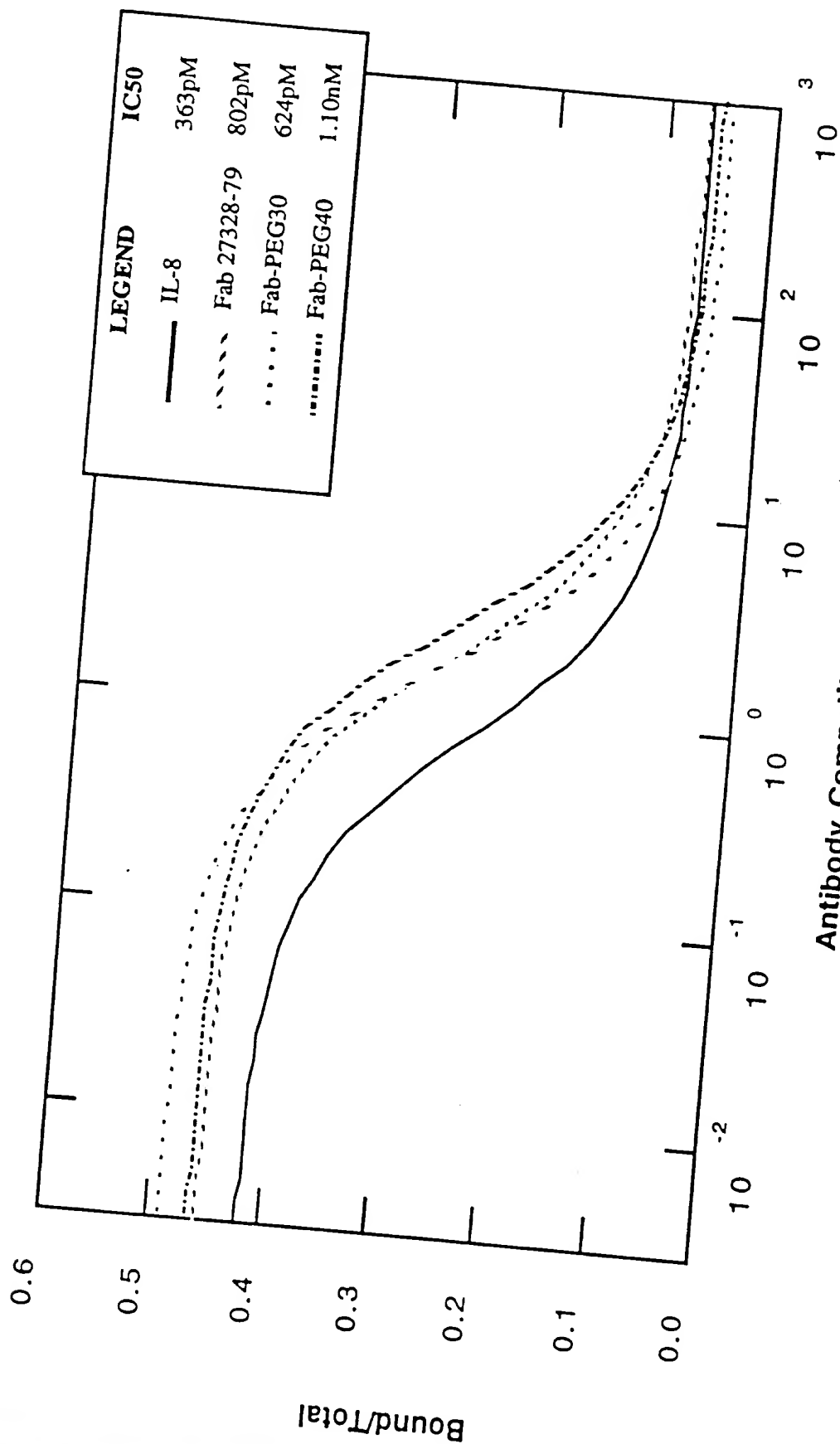
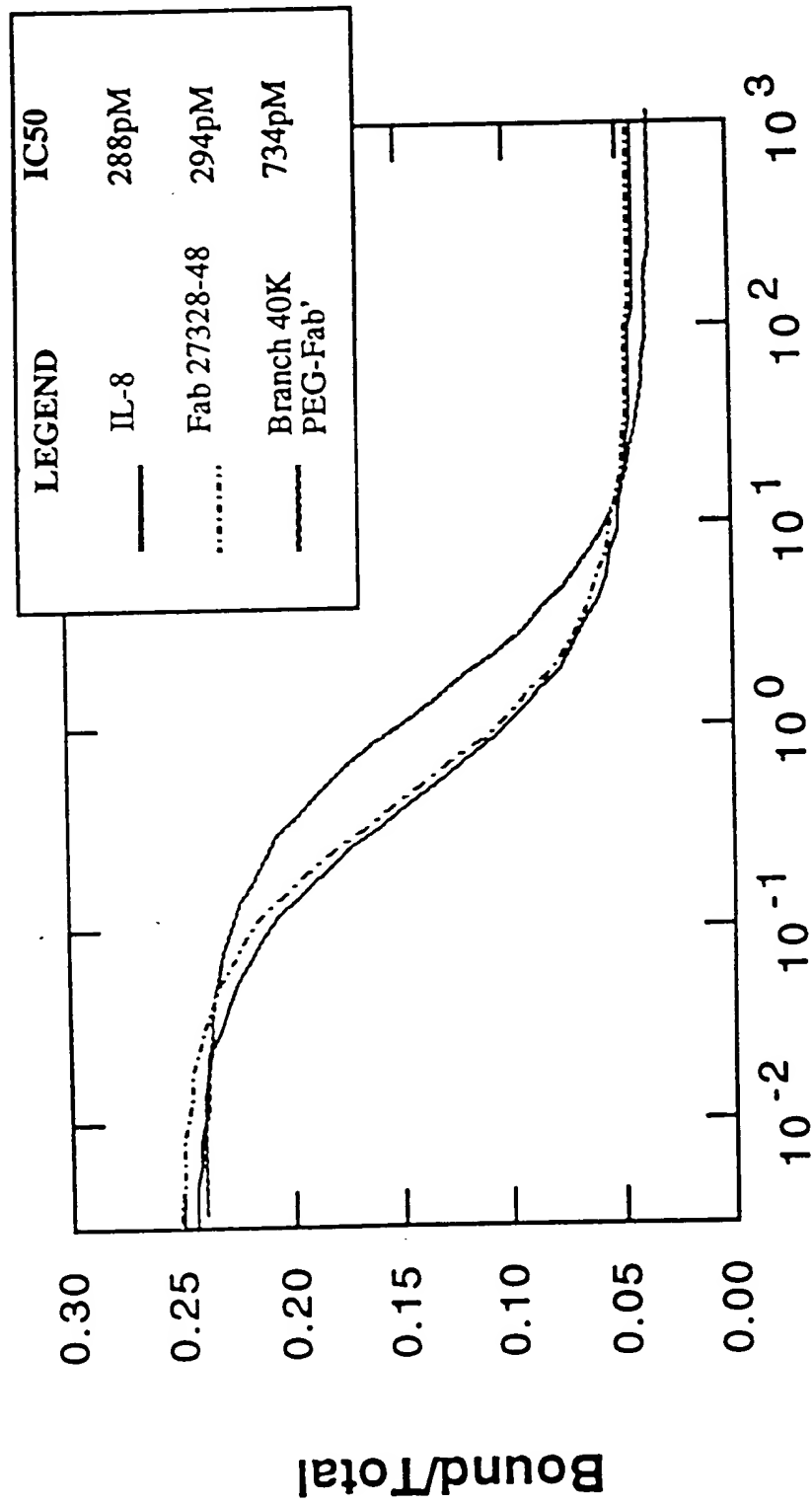


FIG. 54B



Antibody Competitor (nM)

FIG. 54C

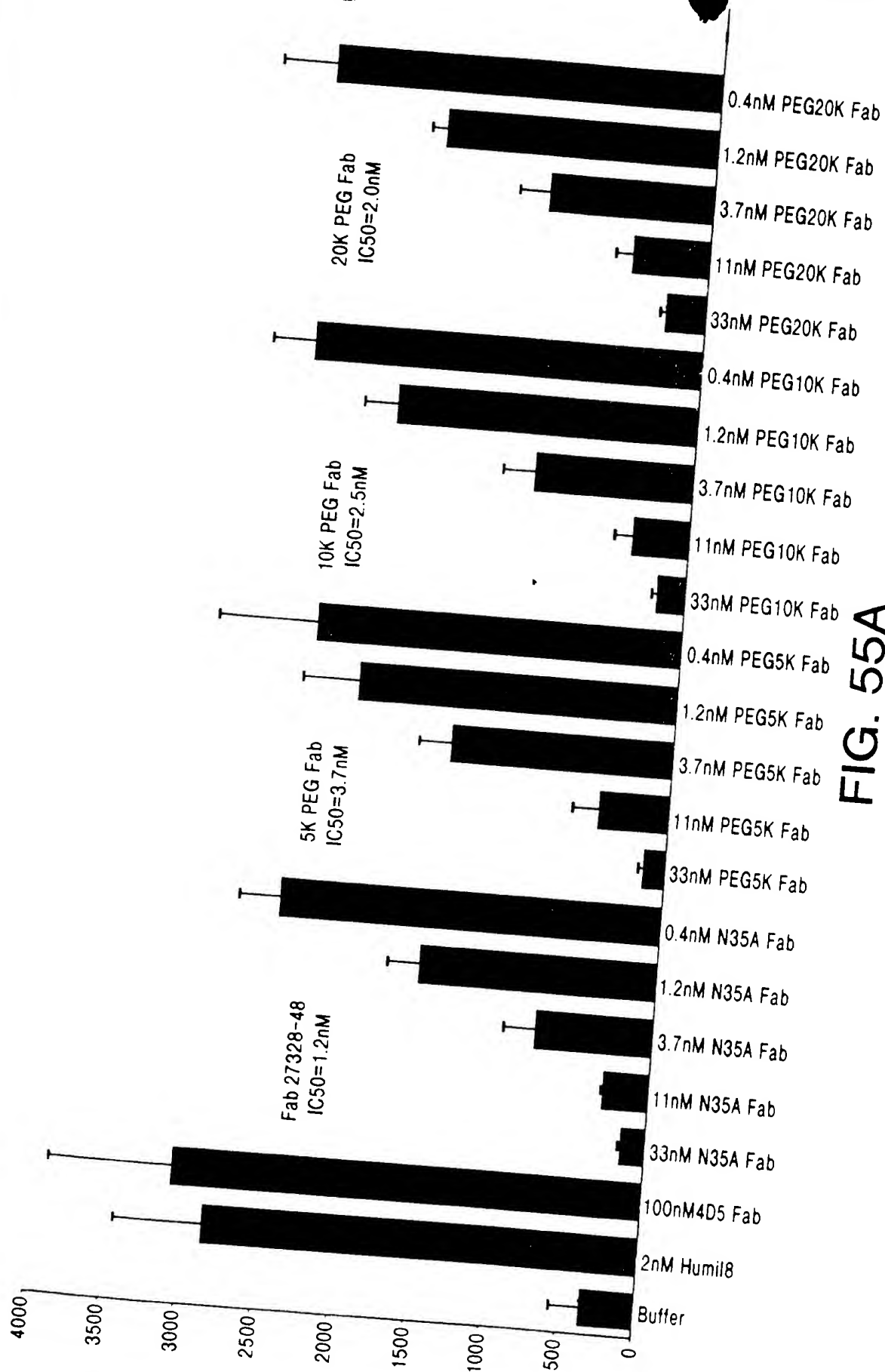


FIG. 55A

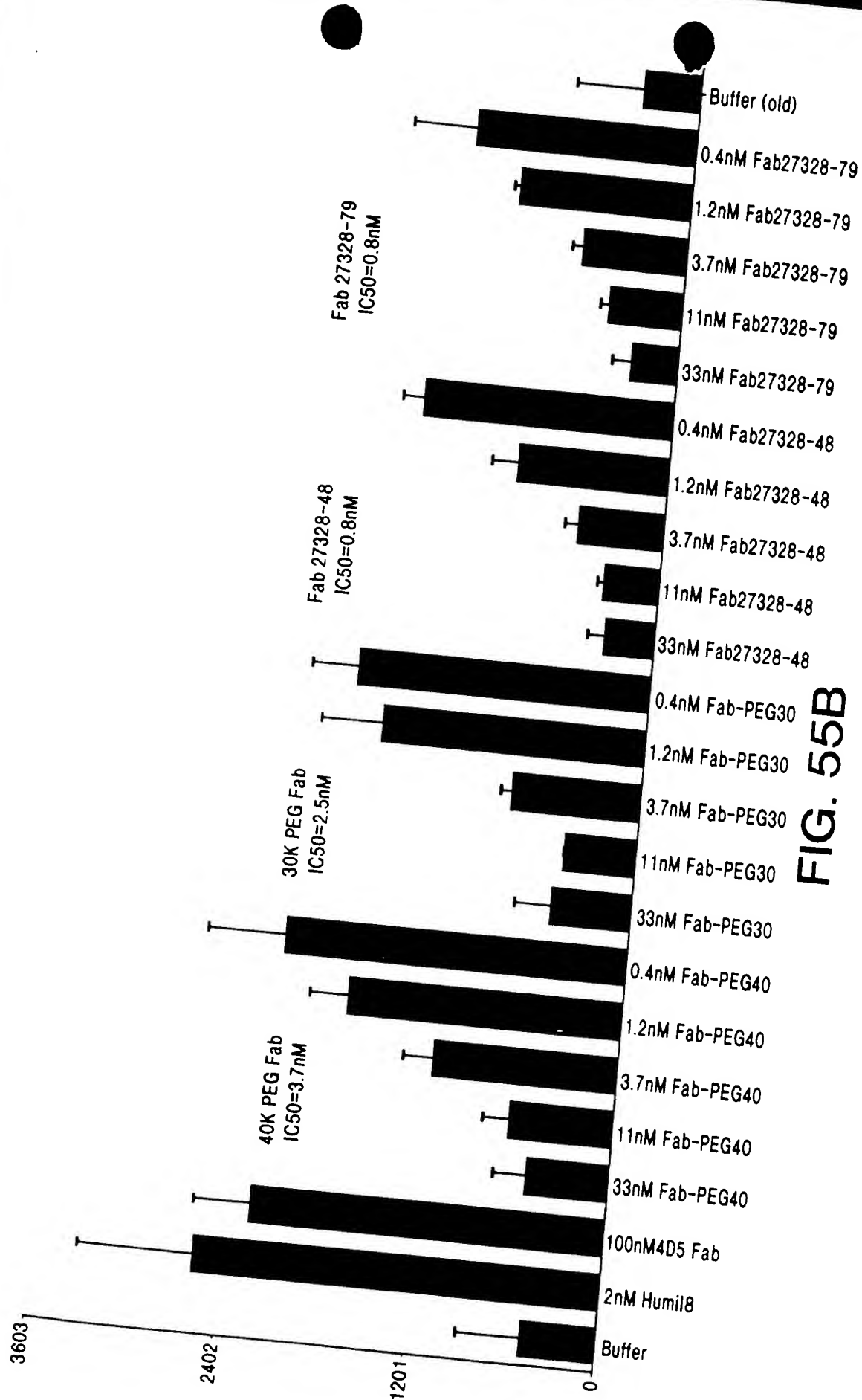


FIG. 55B

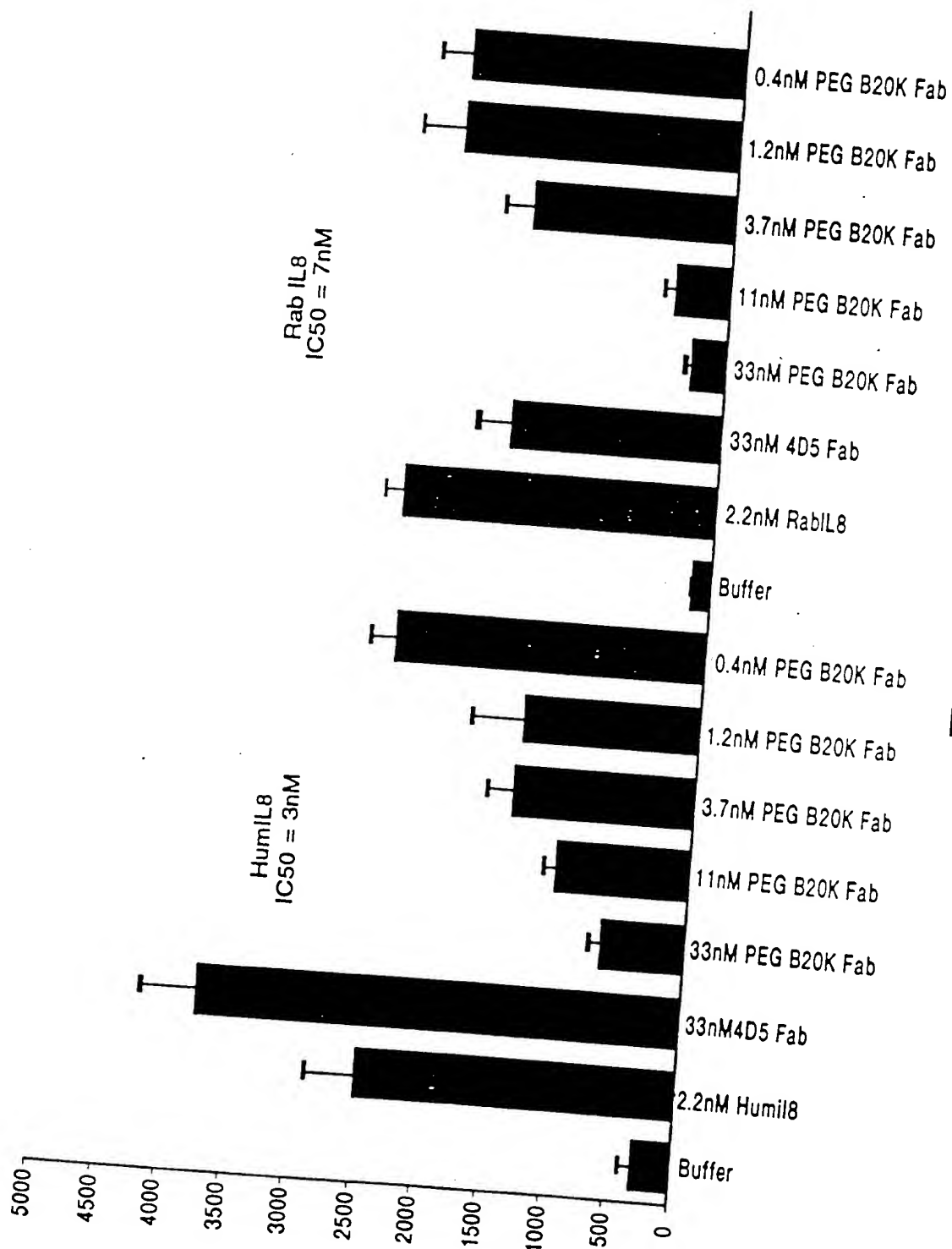
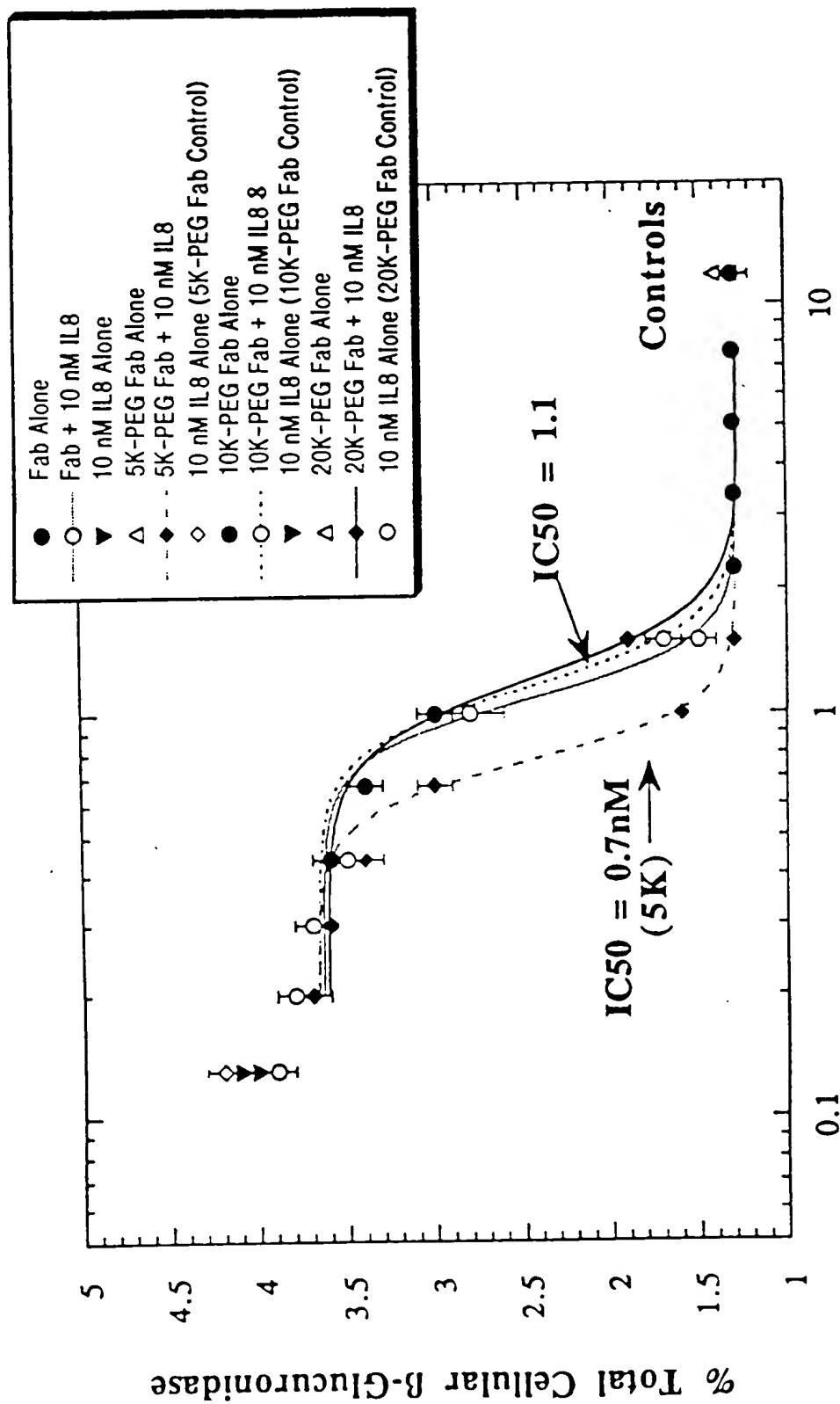


FIG. 55C



Molar Ratio Antibody:IL-8

FIG. 56A

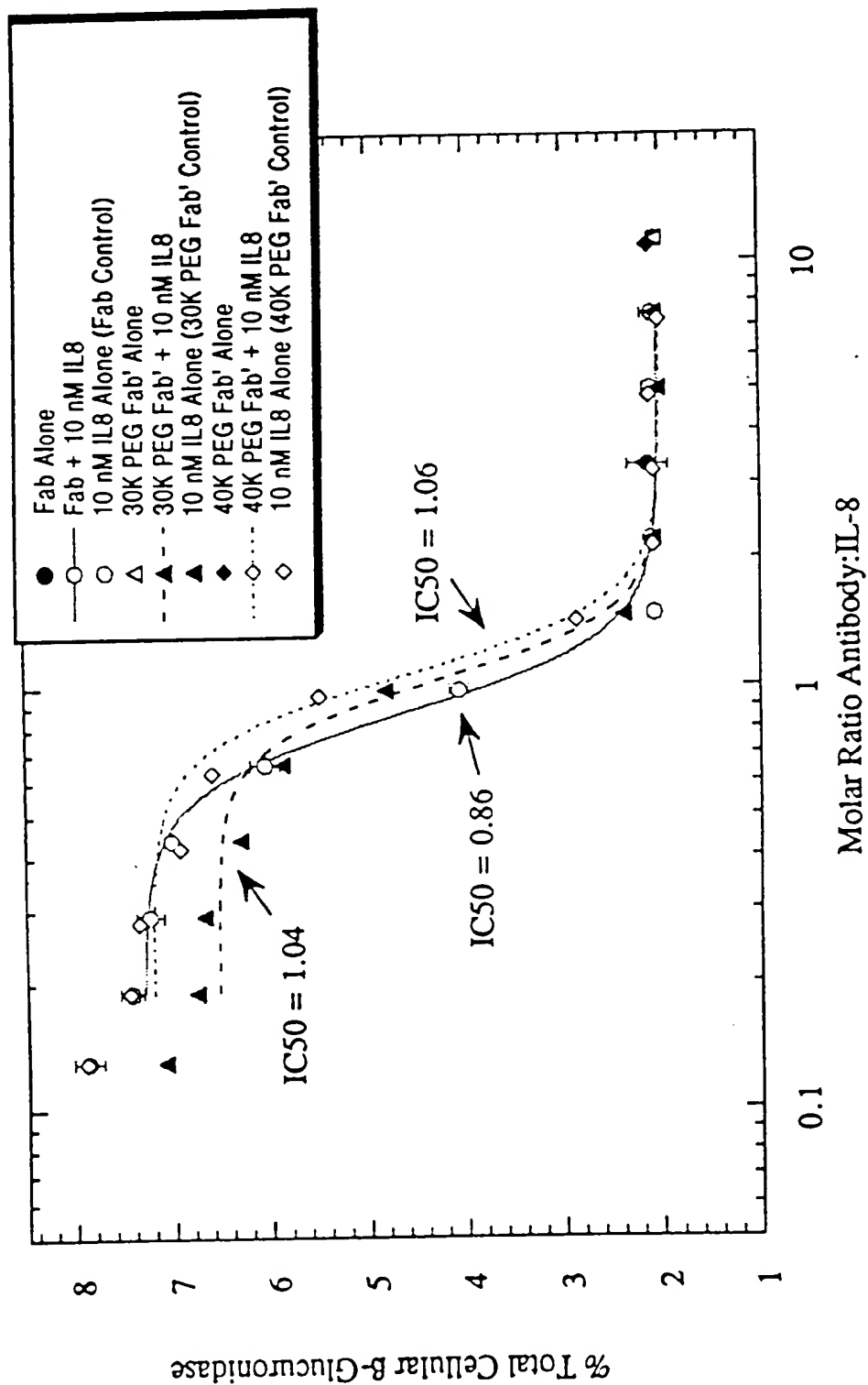
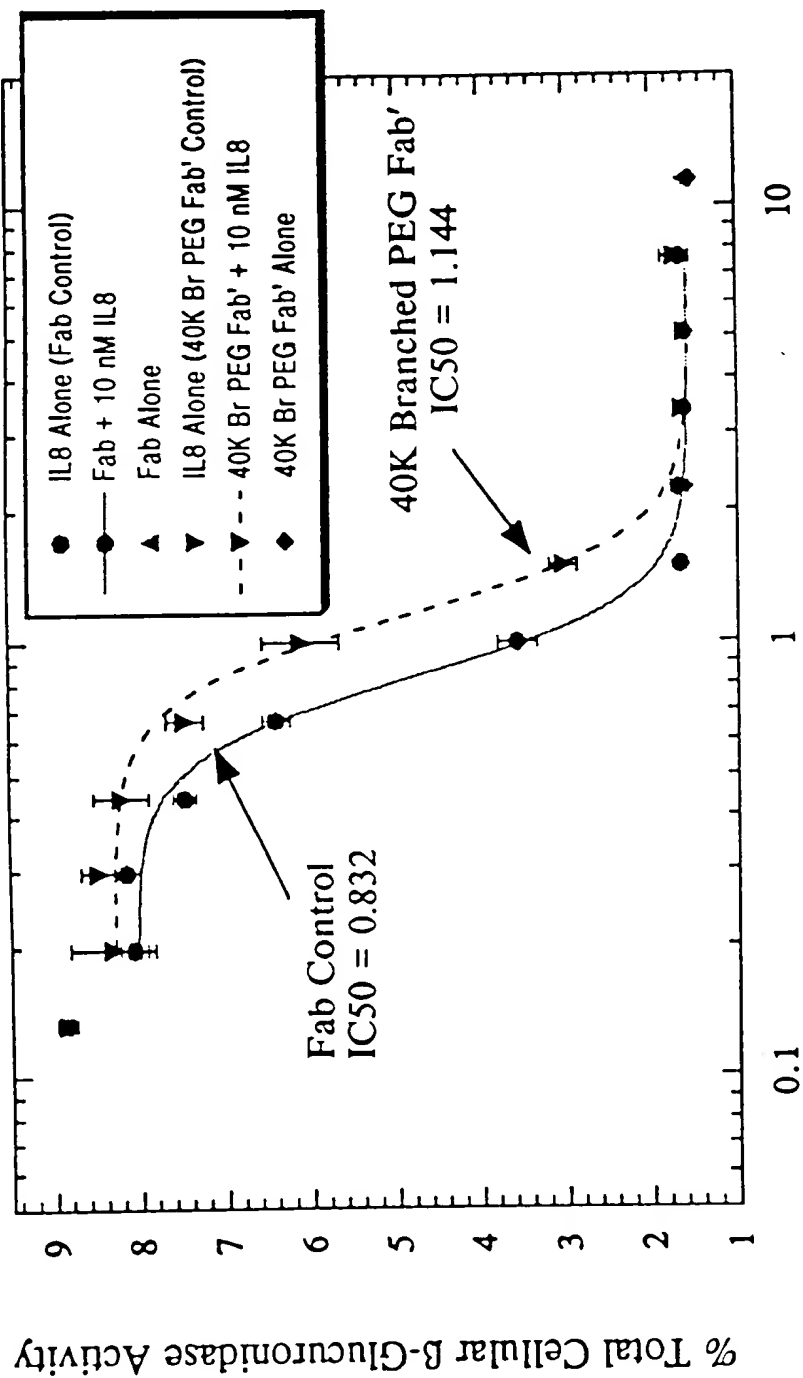


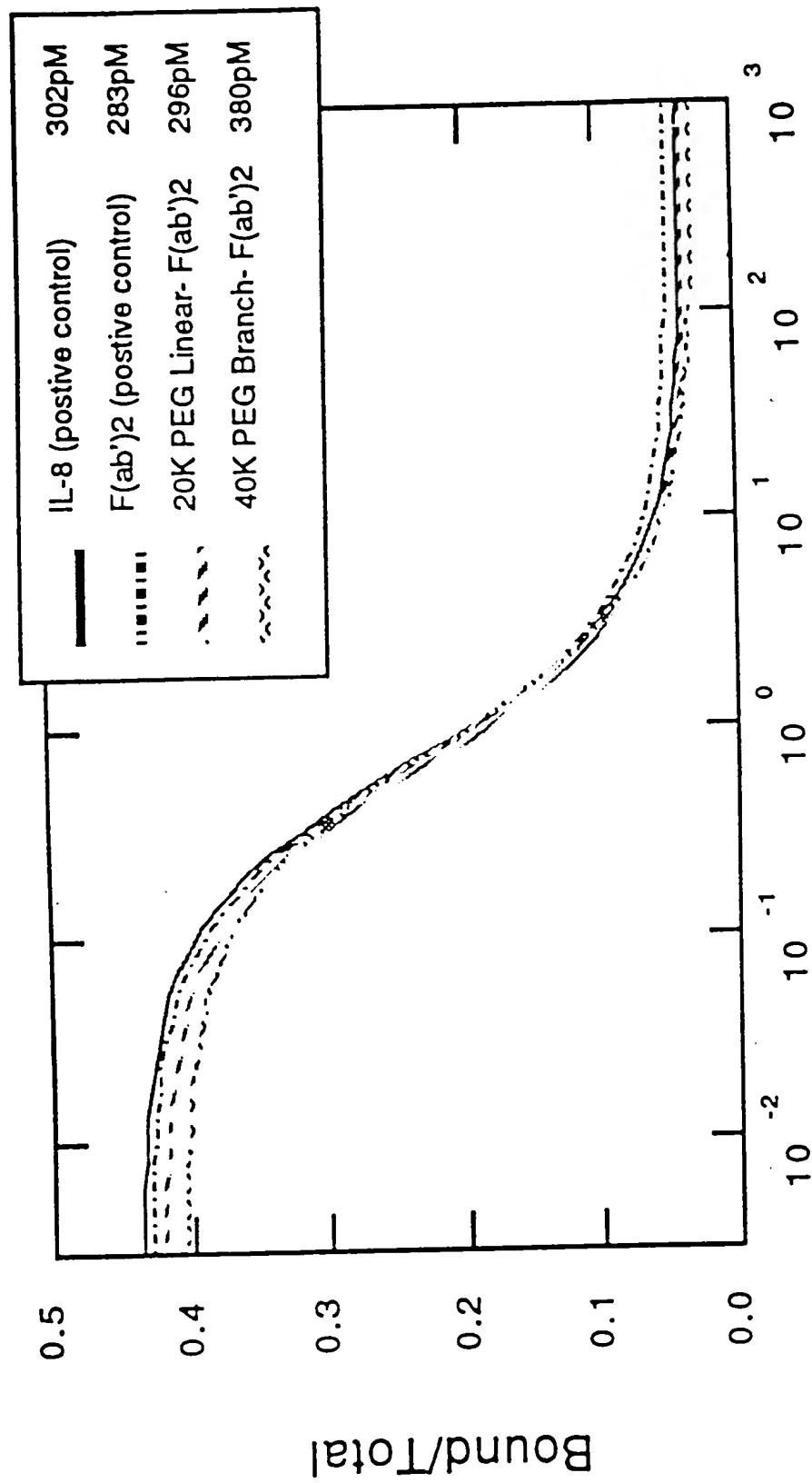
FIG. 56B





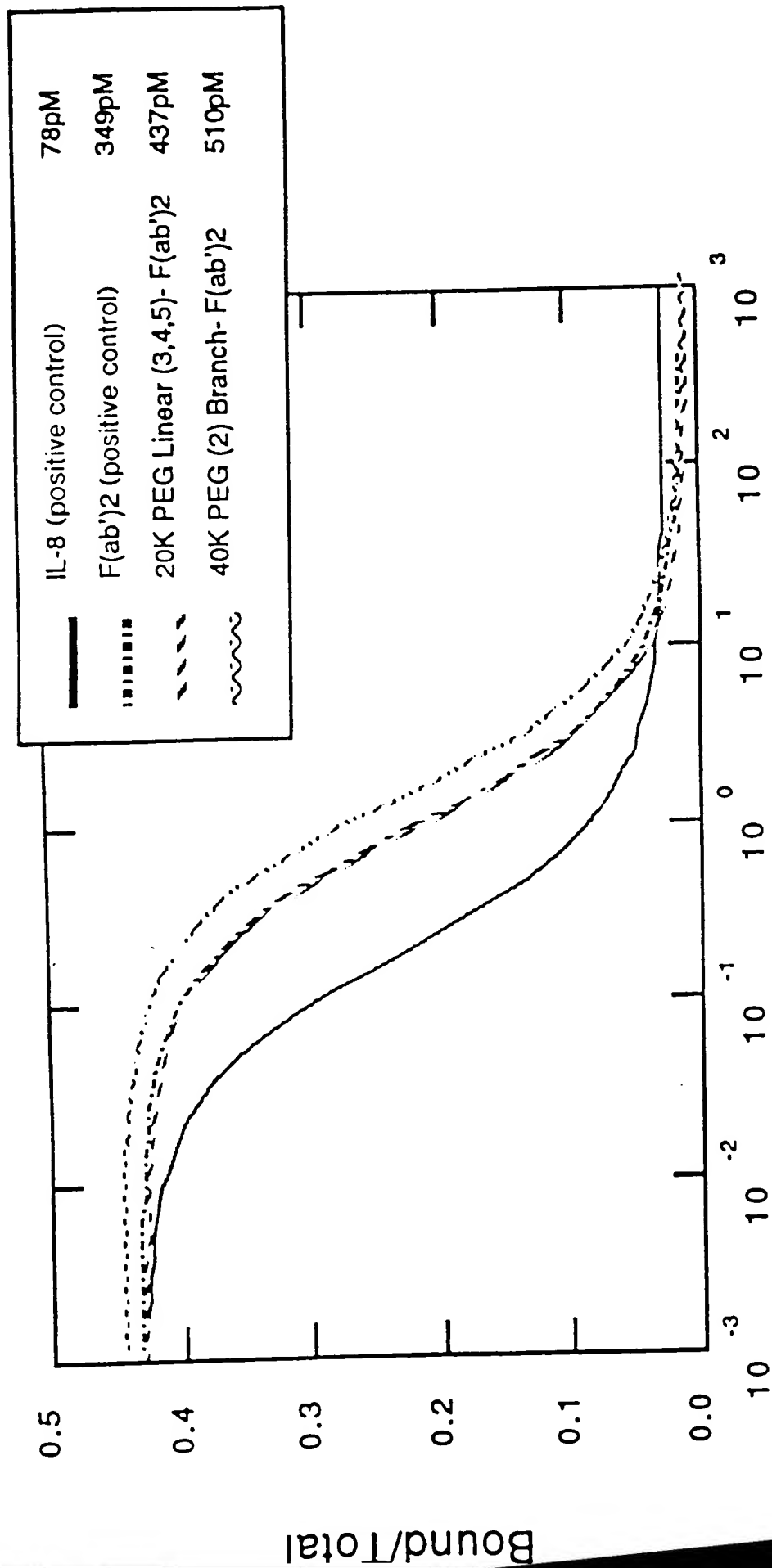
Molar Ratio Antibody:IL8

FIG. 56C



Pegylated F(ab')<sub>2</sub> (nM)

FIG. 57A



Pegylated F(ab')<sub>2</sub> (nM)

FIG. 57B

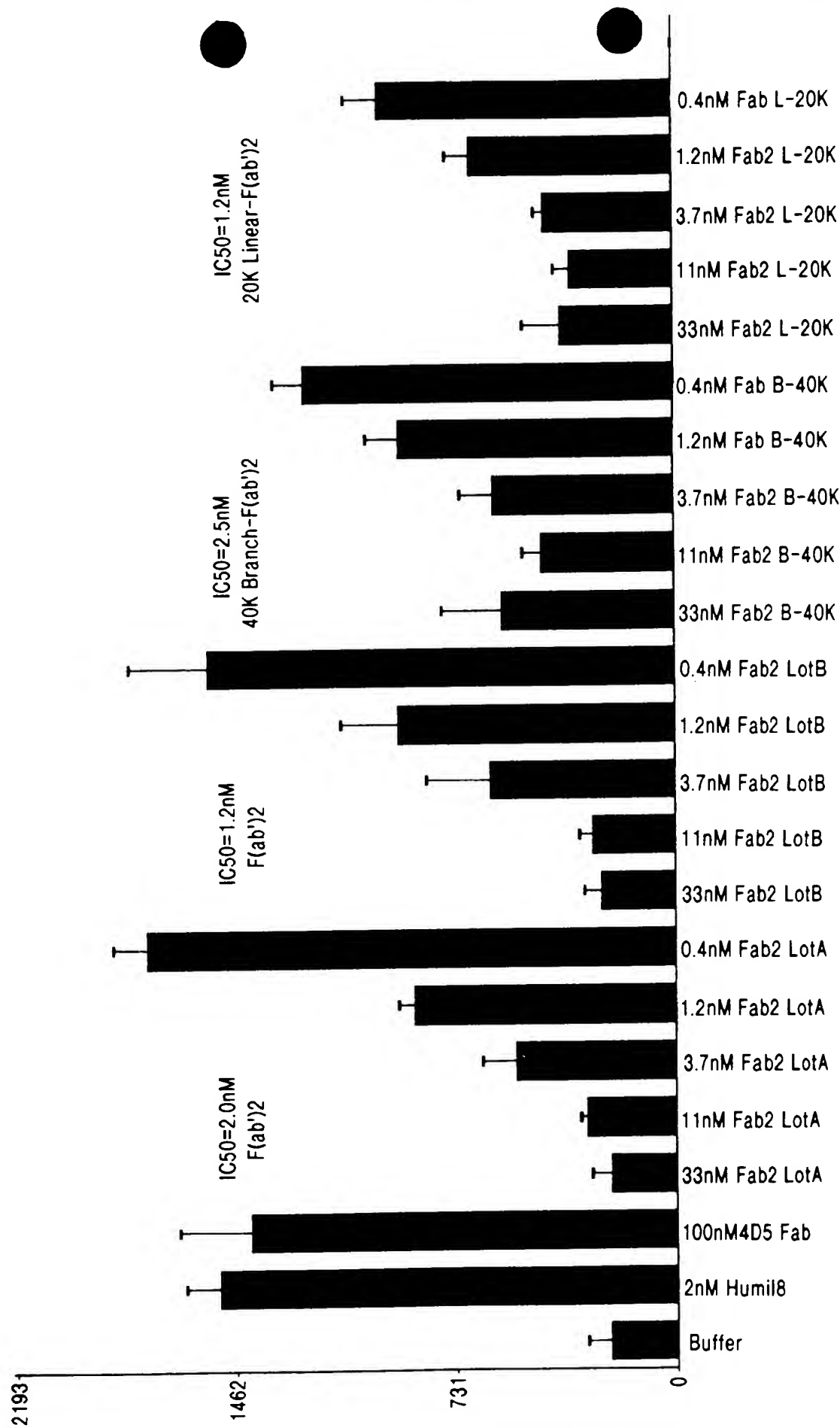


FIG. 58A

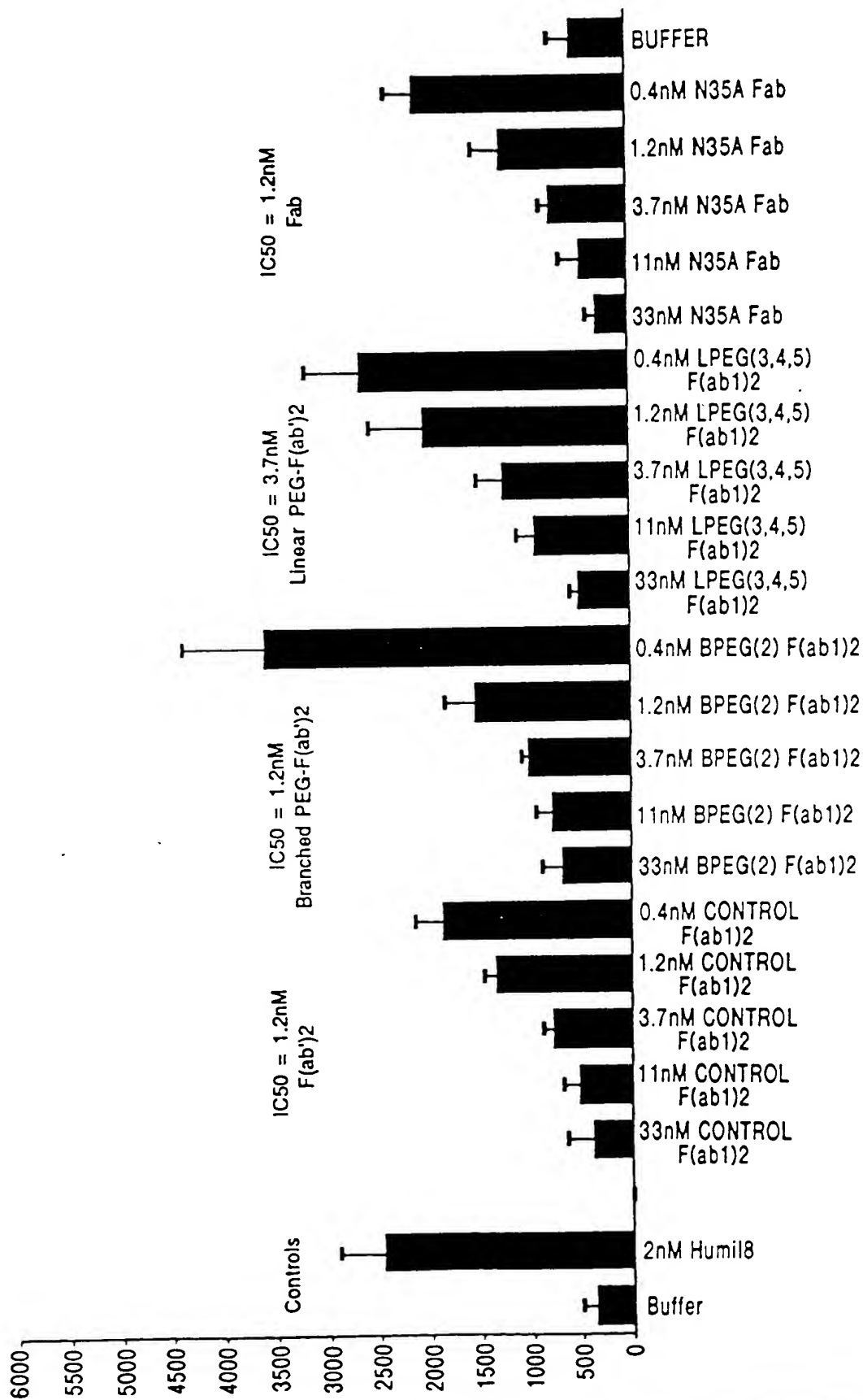


FIG. 58B

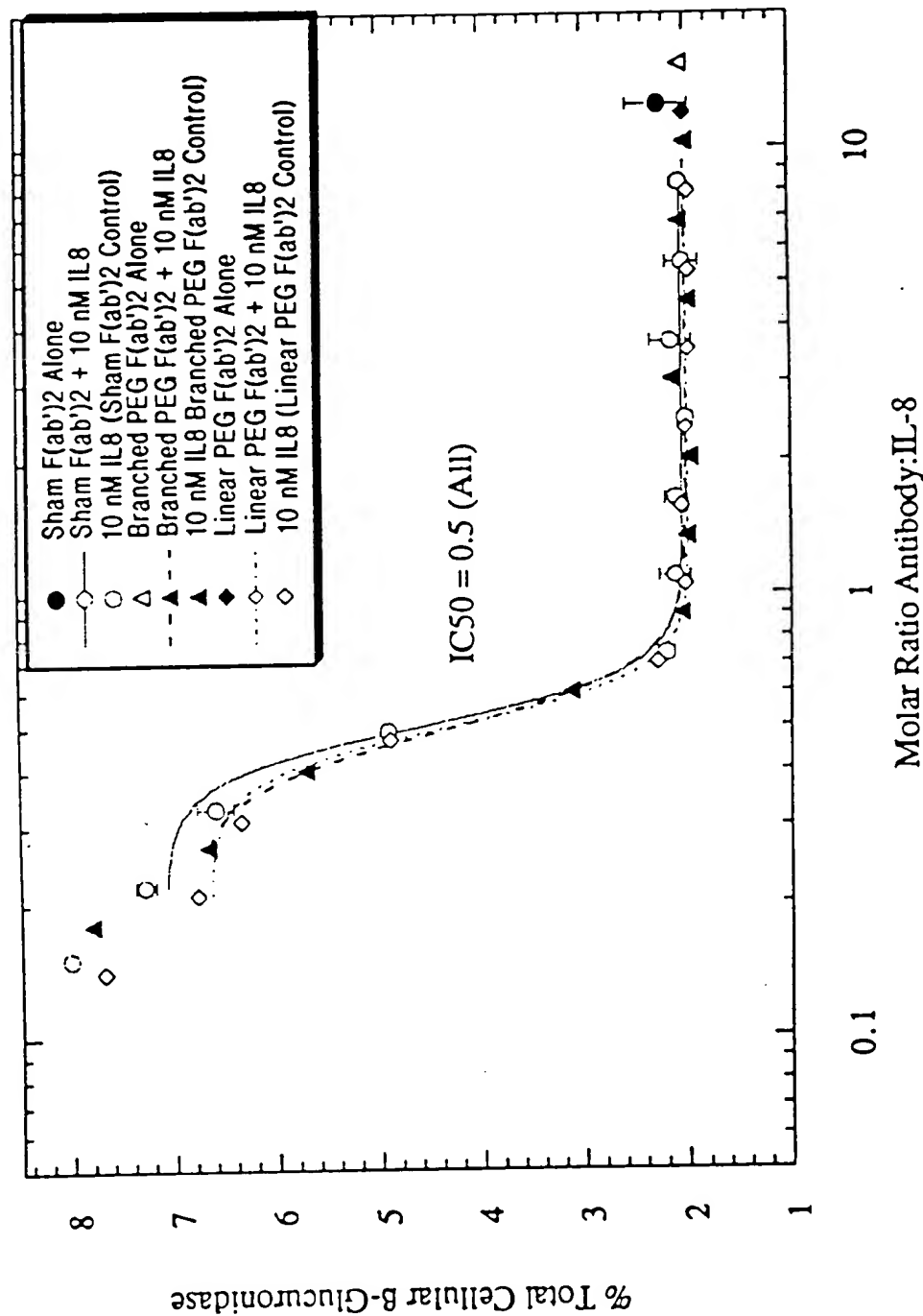
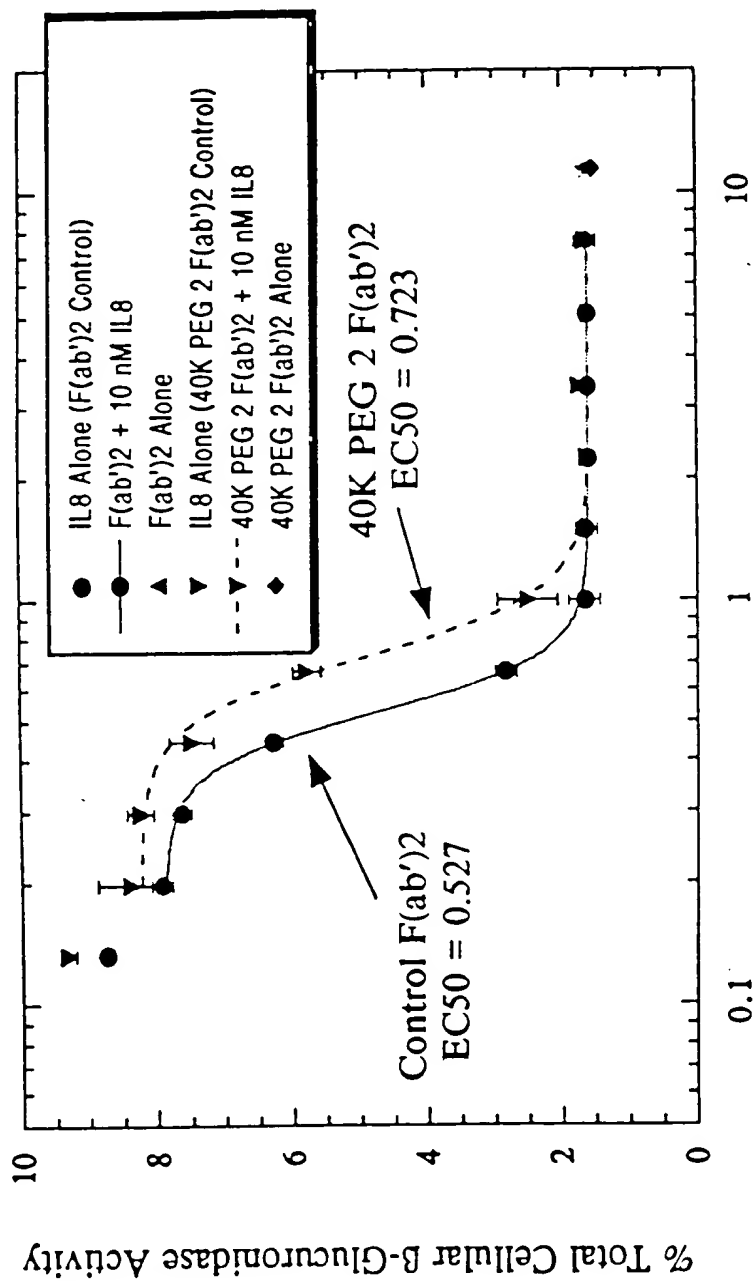


FIG. 59A



Molar Ratio Antibody:IL8

FIG. 59B

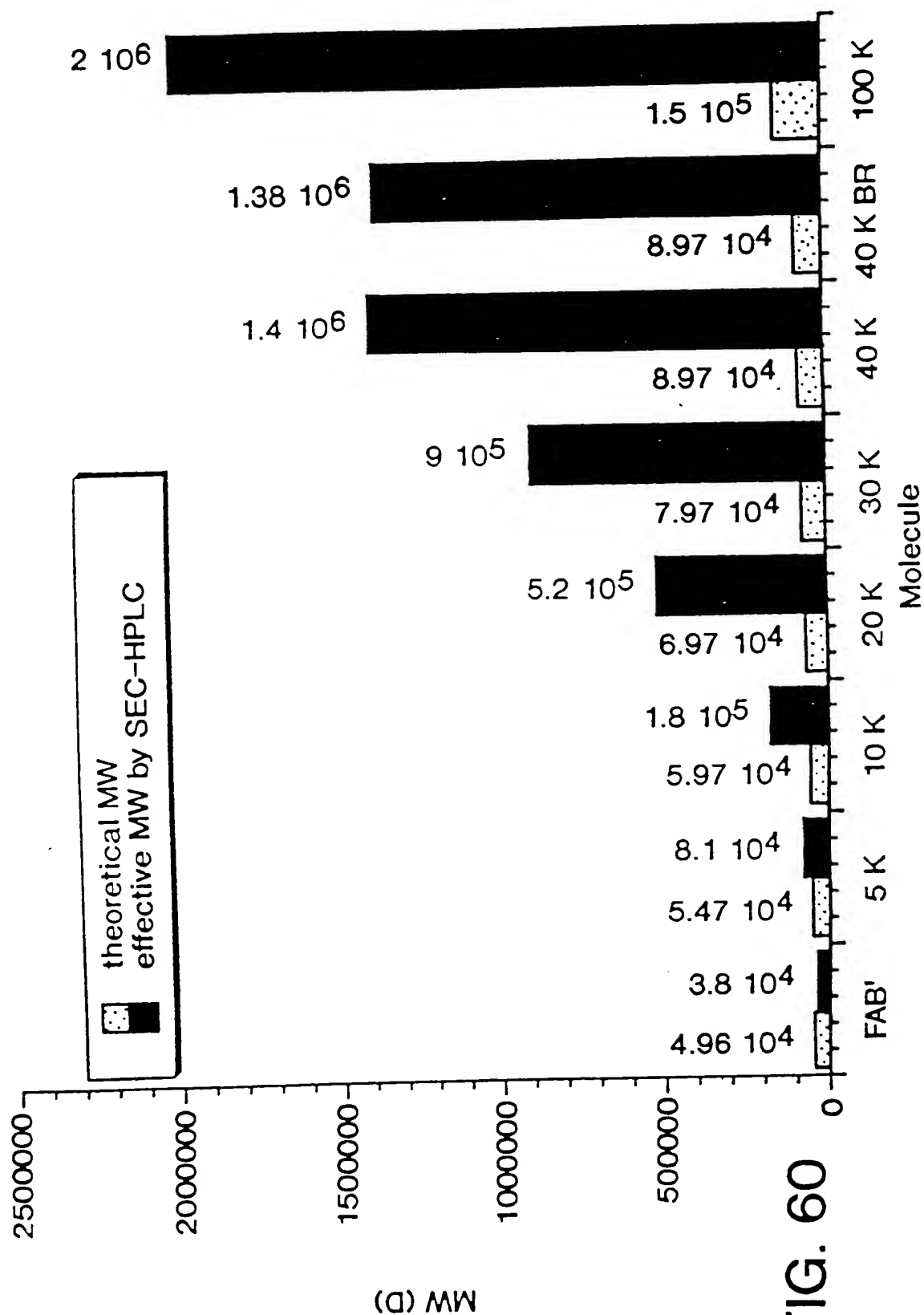
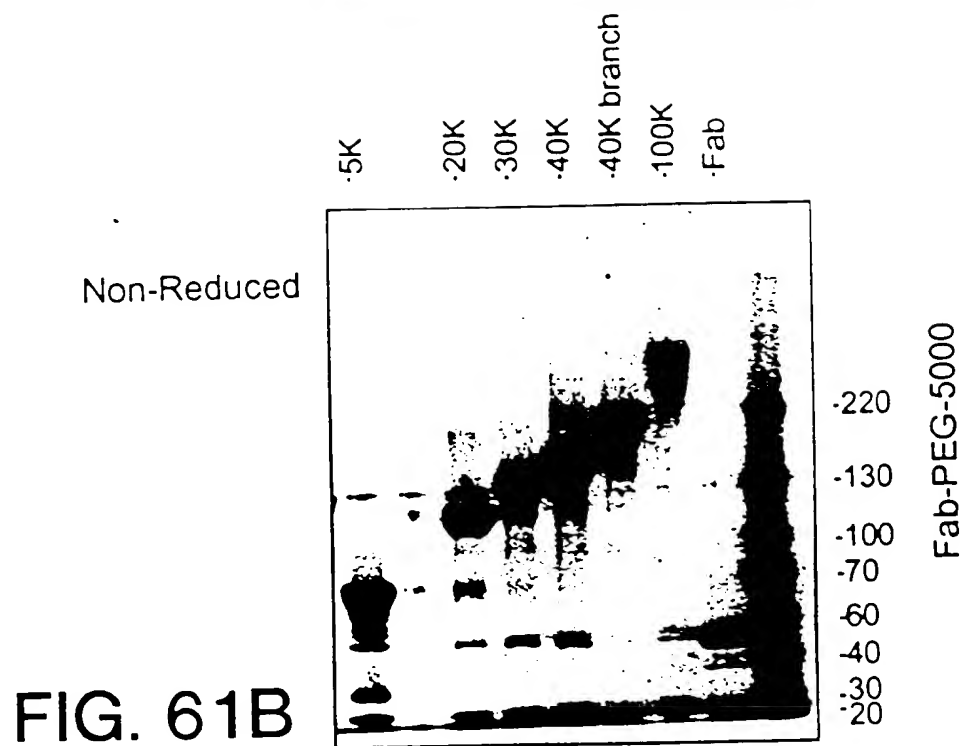
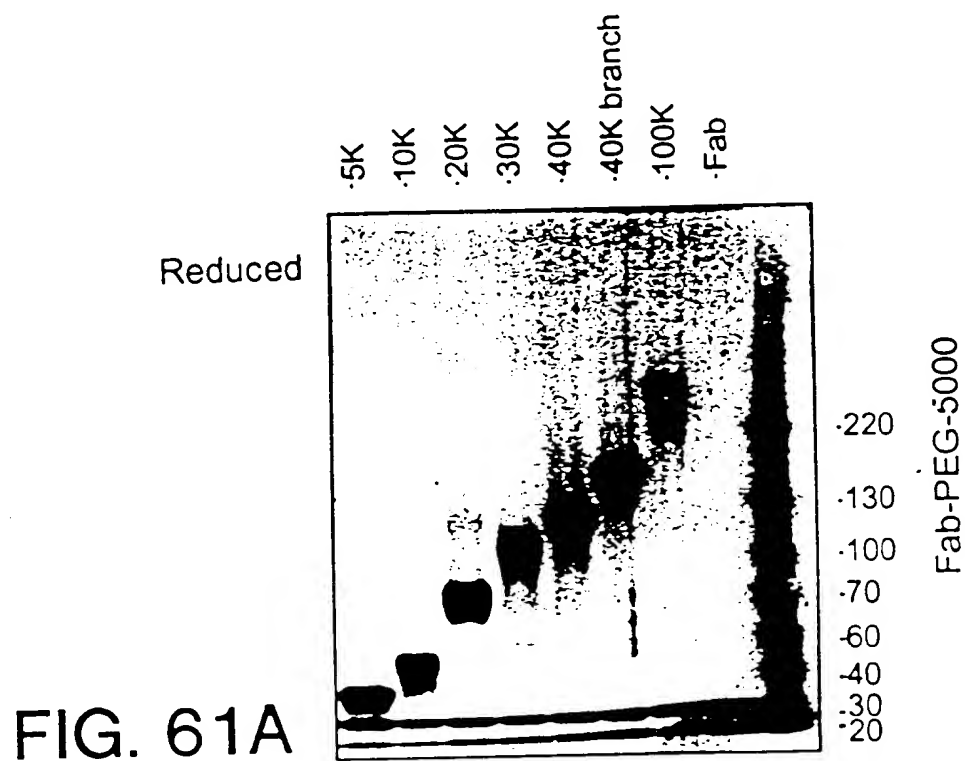


FIG. 60





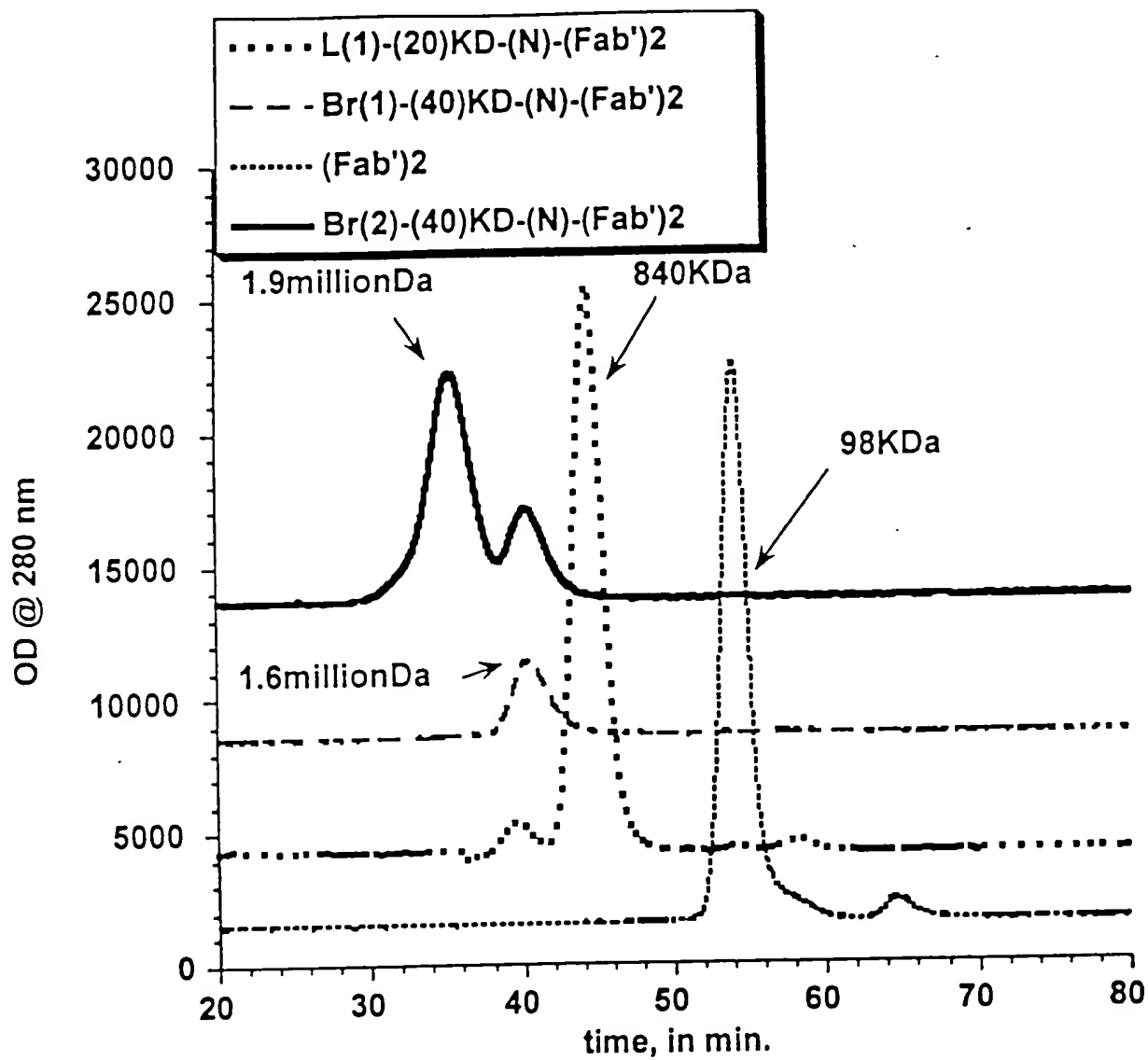


FIG. 62

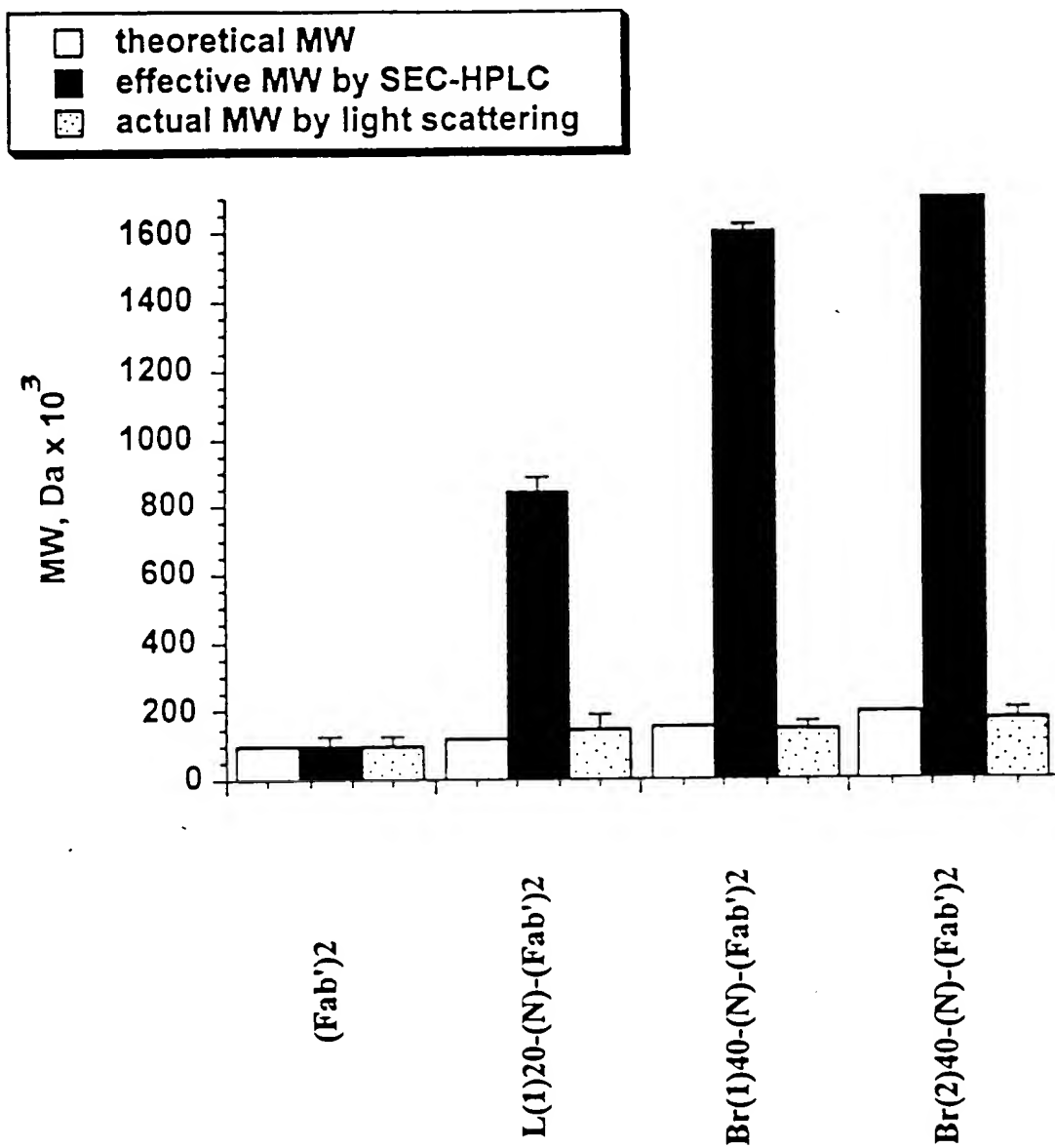


FIG. 63

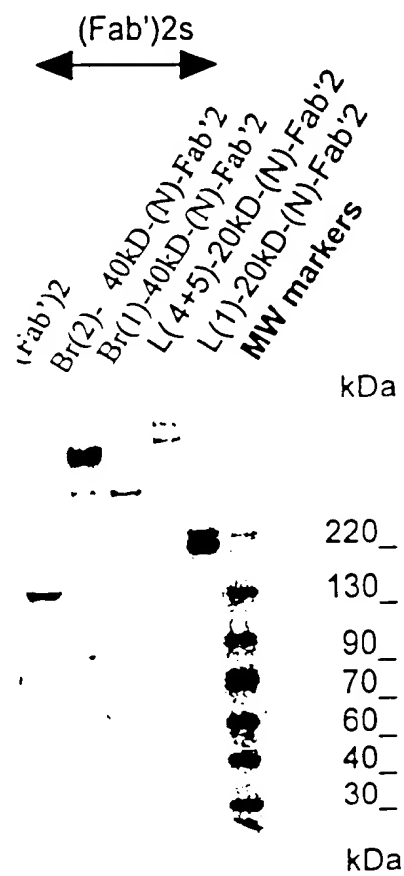
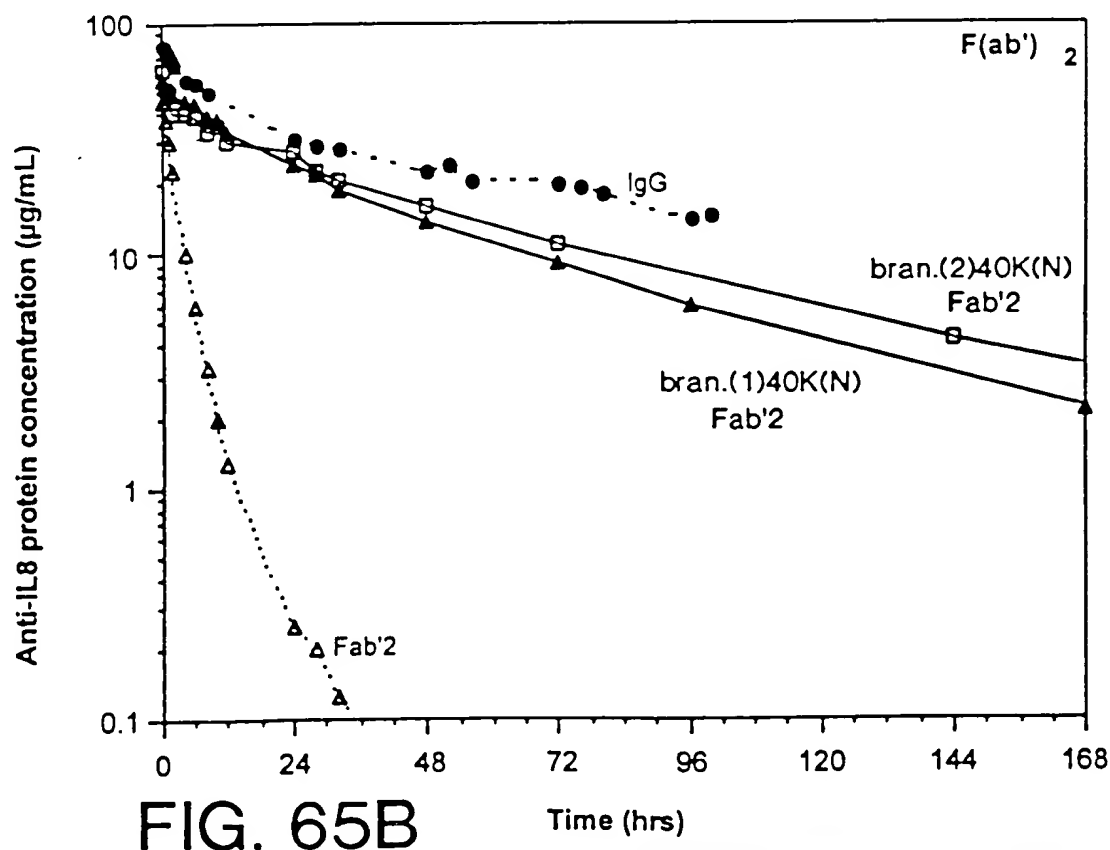
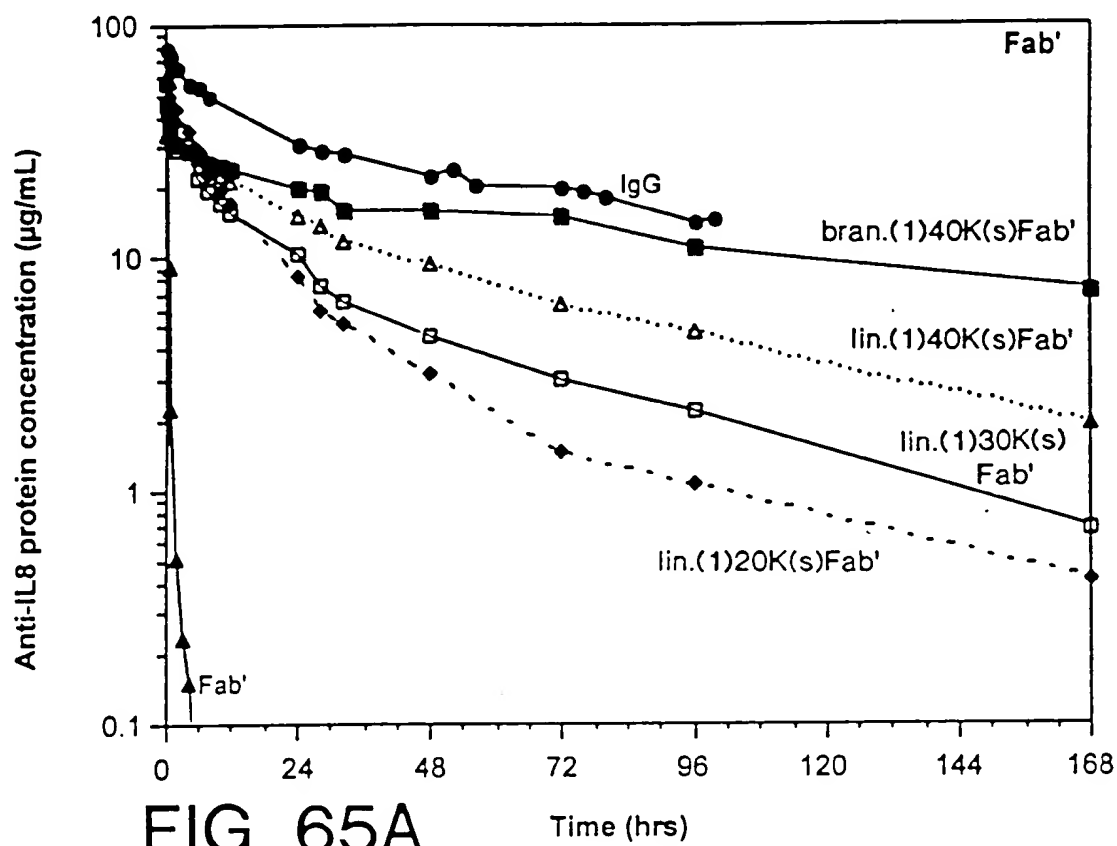


FIG. 64



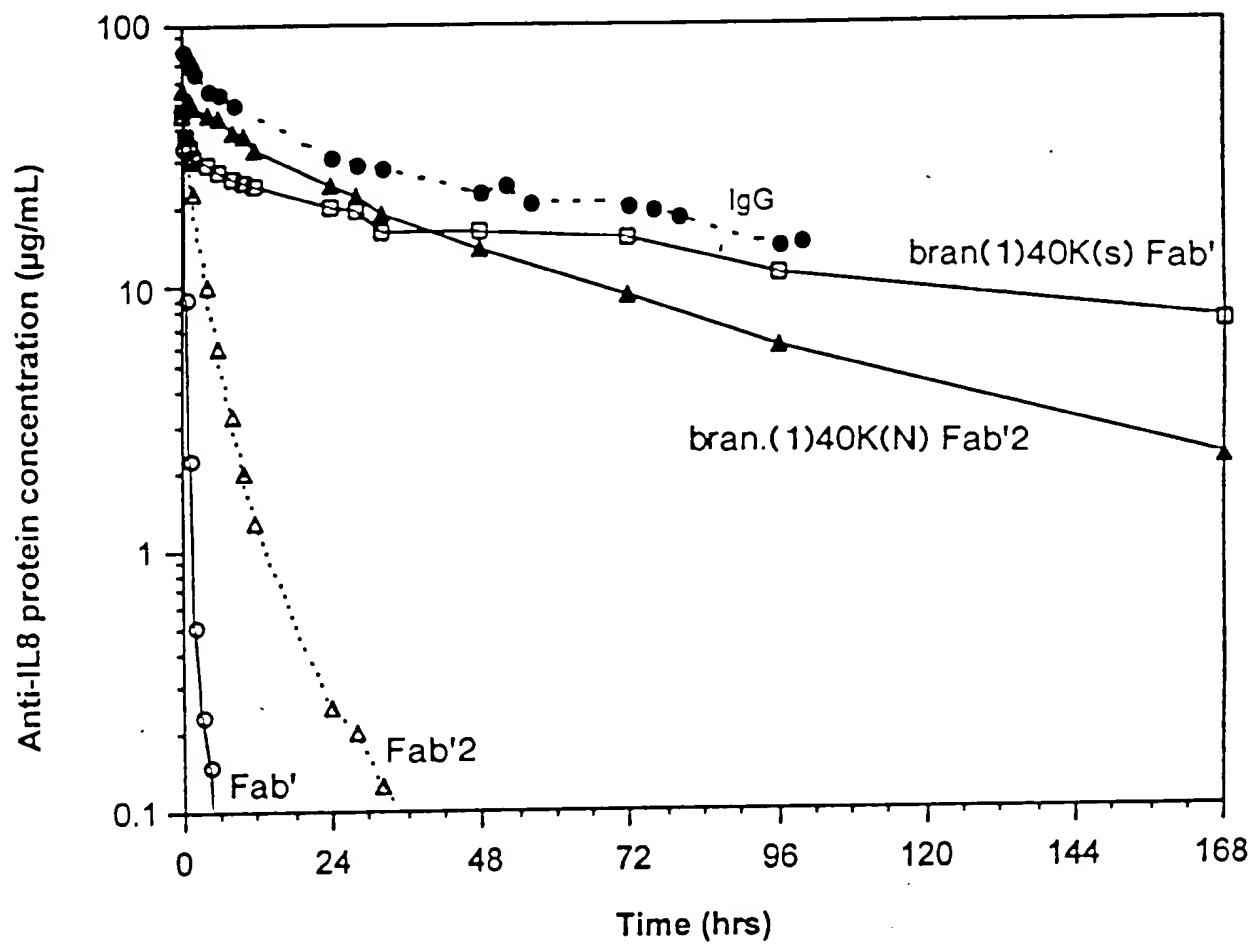


FIG. 66

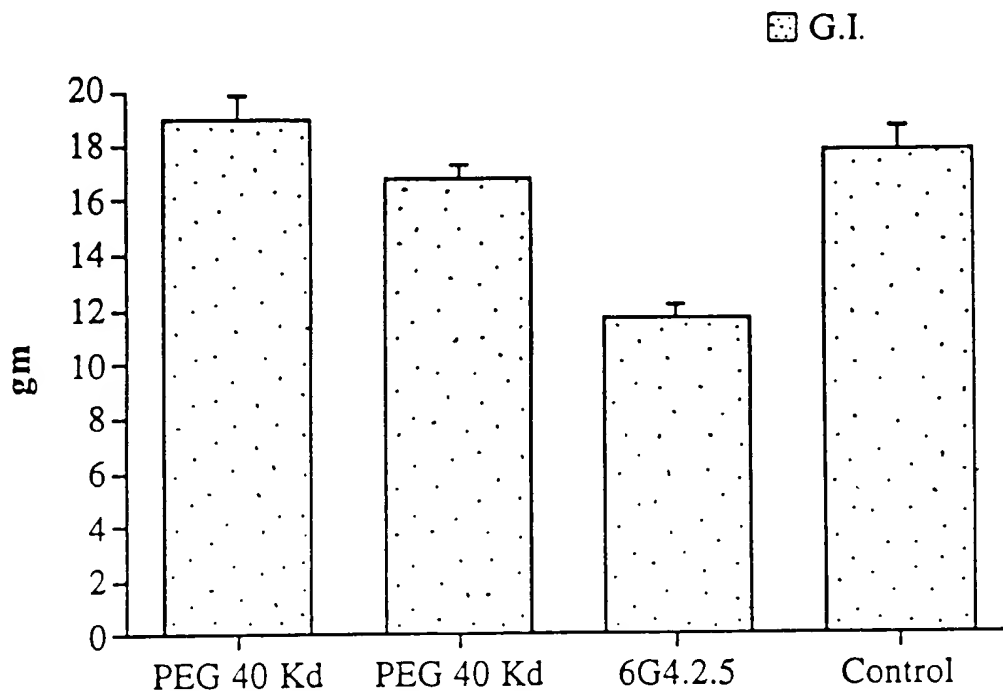


FIG. 67

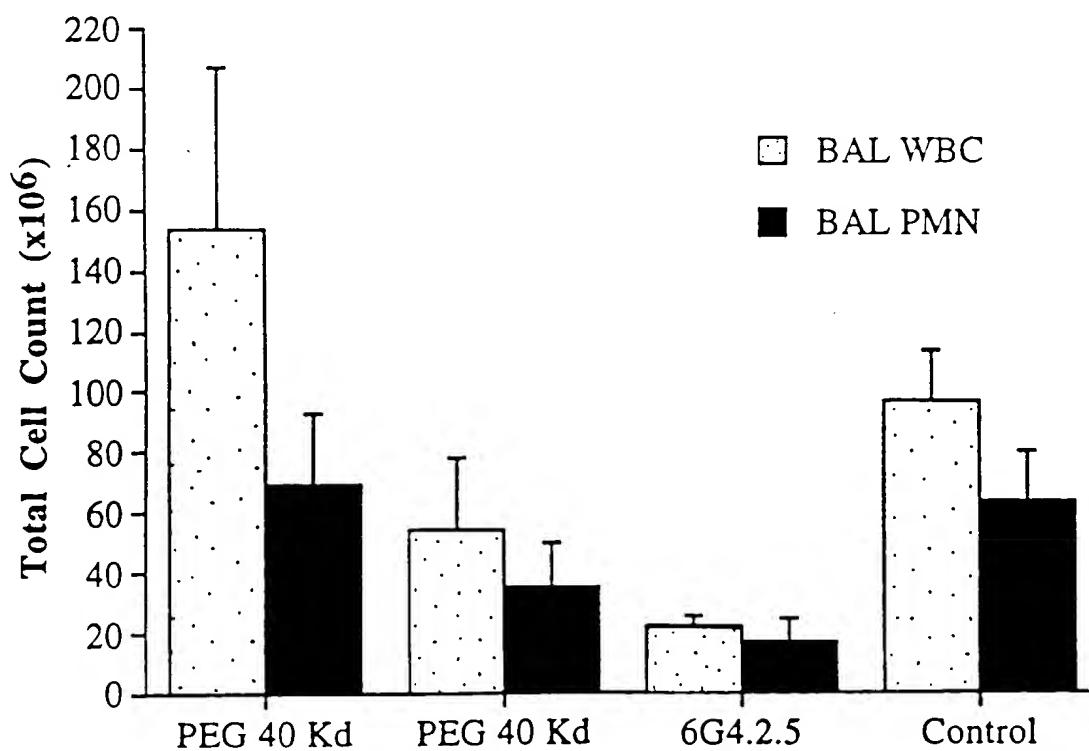


FIG. 68

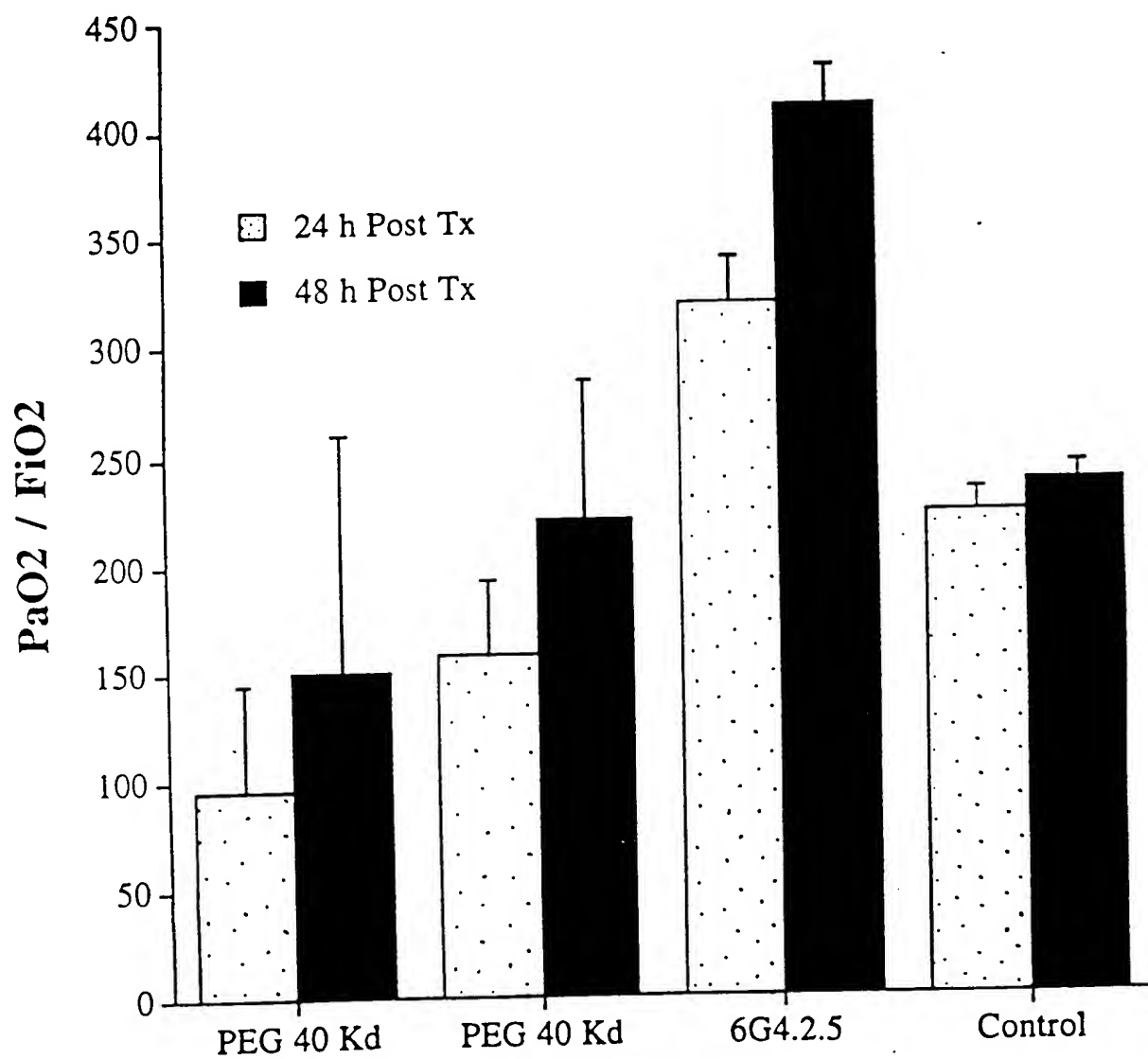


FIG. 69



### Oxygenation in 100% O<sub>2</sub> @24 h Post Anti-IL8 Tx

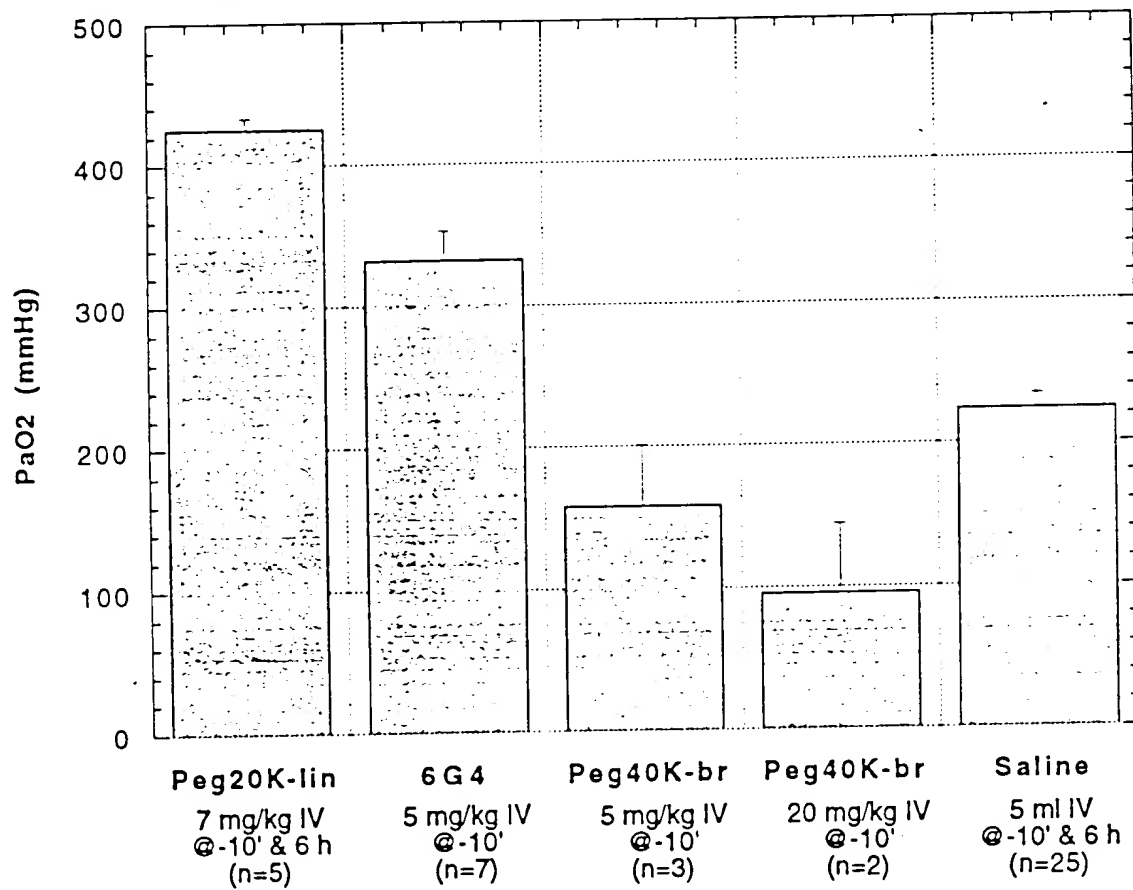


FIG. 70A

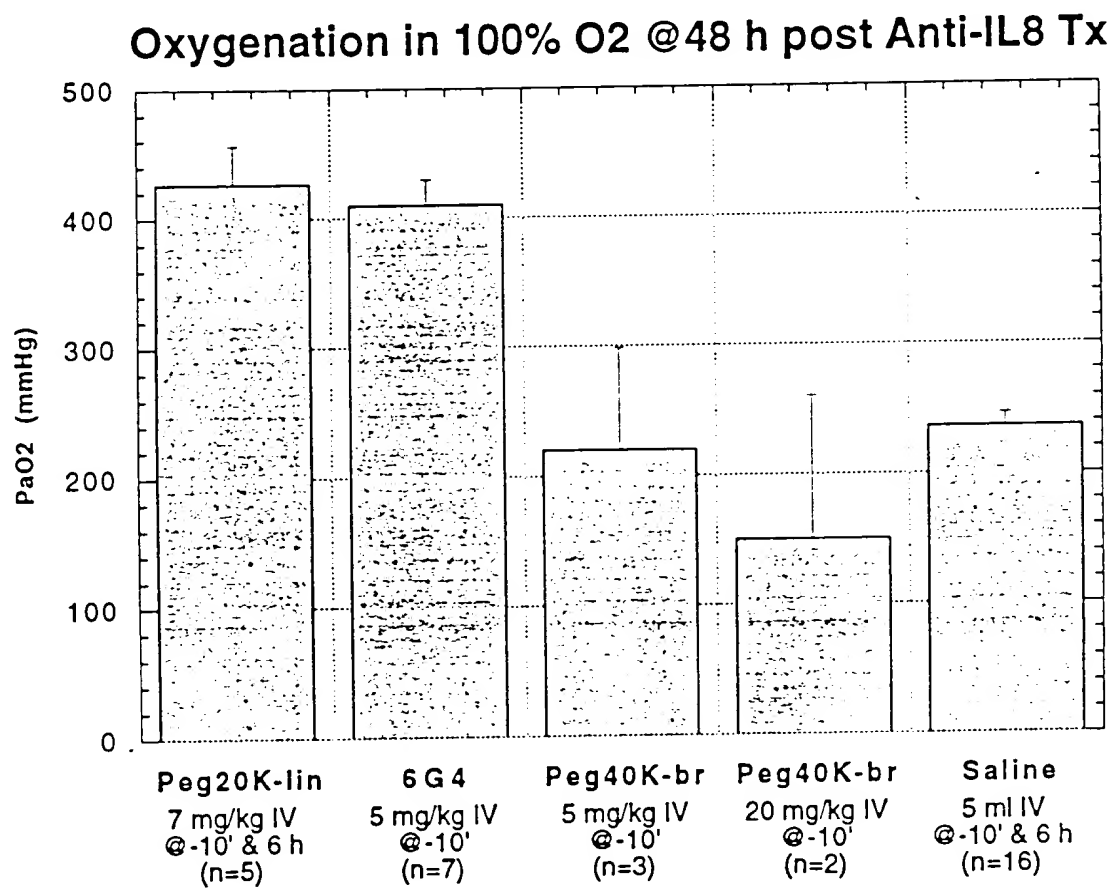


FIG. 70B

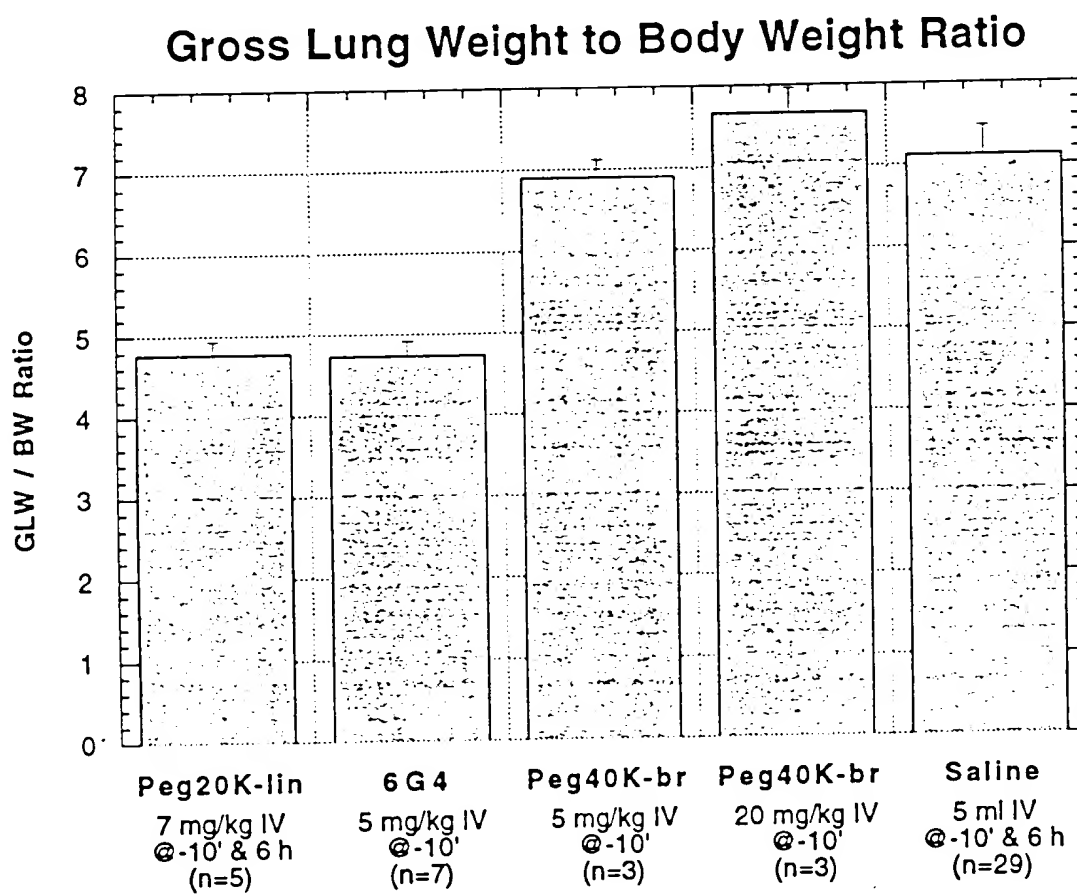


FIG. 70C

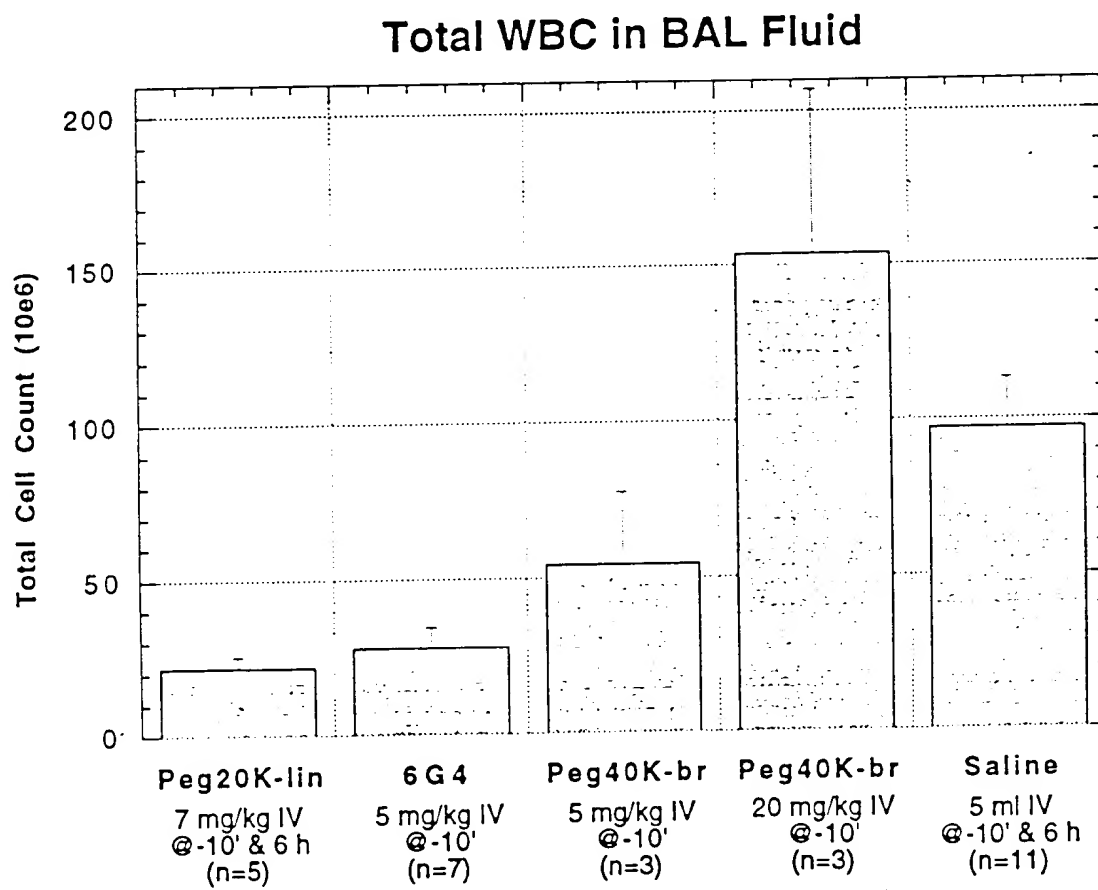


FIG. 70D

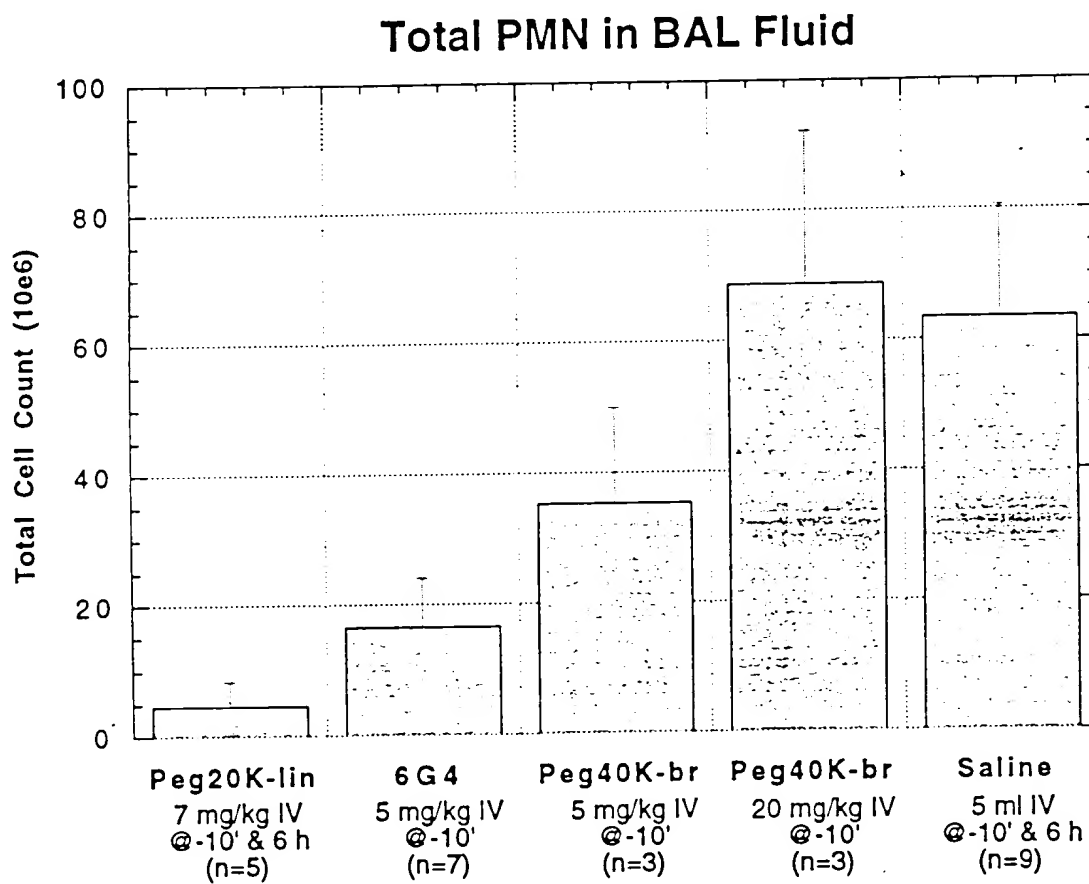
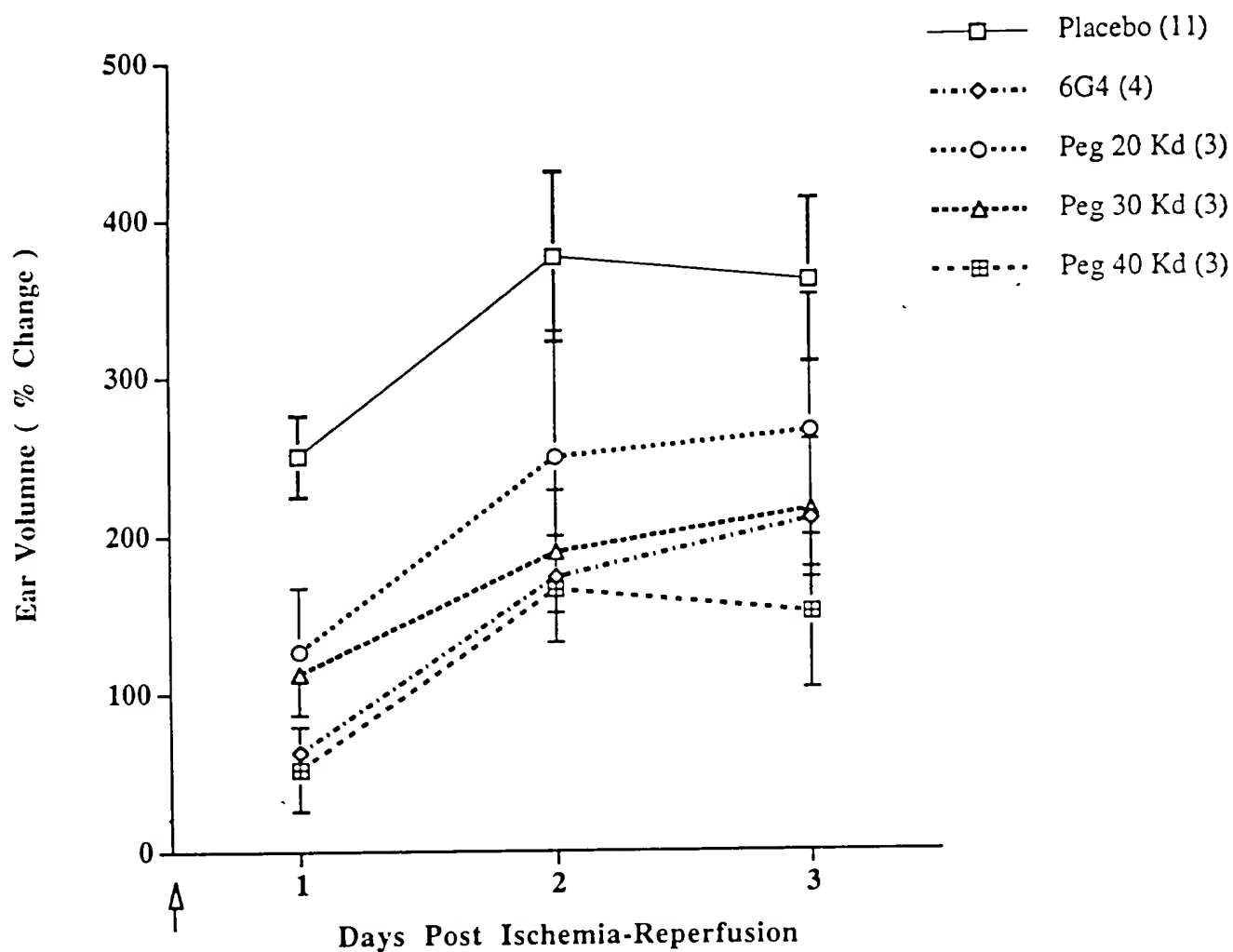


FIG. 70E

## The Effect of Pegylated Anti-IL-8 in the Rabbit Ear model of Ischemia-Reperfusion Injury



Anti-IL-8 formulations :  
Single Dose (5 mg/kg)  
administered IV at time  
of reperfusion

FIG. 71